

## STIC Search Report Biotech-Chem Library

## STIC Database Tracking Number 115431

TO: Diana Johannsen

Location: REM/2C85

Art Unit: 1634

Monday, March 01, 2004

Case Serial Number: 09692077

From: Toby Port

**Location: Biotech-Chem Library** 

Remsen 1A59

Phone: 571-272-2523

toby.port@uspto.gov

## Search Notes

Dear Examiner Johannsen,

Here are the results of your search.

Please feel free to contact me if you have any questions.

**Toby Port** 



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# STIC SEARCH RESULTS FEEDBACK FORM

## Biotech-Chem Librain

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 571-272-2507 Remsen E01 D86

Vol	luntary Results Feedback Collins							
A	I am an examiner in Workgroup: Example: 1610							
>	Relevant prior art found, search results used as follows:							
	☐ 102 rejection							
	☐ 103 rejection							
	Cited as being of interest.							
	Helped examiner better understand the invention.							
	☐ Helped examiner better understand the state of the art in their technology.							
	Types of relevant prior art found:							
	☐ Foreign Patent(s)							
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)							
>	Relevant prior art not found:							
	Results verified the lack of relevant prior art (helped determine patentability).							
	Results were not useful in determining patentability or understanding the invention.							
Cor	mments:							

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	/gene="ADRA2C" /codon_start=1 /product: "alpha-2-adrenergic receptor" /product: "alpha-2-adrenergic receptor" /product: "alpha-2-adrenergic receptor" /protein_id="AAA62823.1" /db_xref="GI:177868" /db_xref="GI:177868" /db_xref="GI:177868" /db_xref="GI:177868" /translation="FCTSSIVHLCAISLDRYWAVSRALEYNSKRTPRRIKCIILTVWLLAKTSISLPPLYKGDQGPQFRGRPQCKLNQERWYILASSIGSFFAPCLIMILVYLRIY LAAVISLPPLYKGGPGQGSSKQAFPQCKLNQERWYILASSIGSFFAPCLIMILVYLRIY EKEEGETPEDTGTRALPSWAALPNSGQGQKGGVCCASPEDEAEEEEEEEEEEEEEEEF GAVPVBPASACSPPLQOPQGSRVLATLRGQVLLGRGVGGAIGGQWWRRRAQUTREKKFT FVLAVVIGVFVLCWFPFFF"	/9ene="ADRA2C" 1885	/organism="Homo mapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /map="4p16.3-p15" /clone="PCRA2" /cell_line="neuroblastoma SK-N-SH" /cell_type="neuroblastoma" /dev_stage="adult" 1885	11851Tute of Neuroscience 155, Sect II, Li-Noon St. Taipei, Taiwan, 11221 ROC. Location/Qualifiers 1. 885	Bource text: Human adult neuroblast ry and computer-readable sequence f bmitted sequence f	etazoa; Chordata; Craniata; Vertebre theria; Primates; Catarrhini; Homini co 885) fo,T.F. and Chang,N.C. lification by polymerase chain react the third subtype of alpha-2 adren hys. Res. Commun. 172 (2), 817-823		AC135438 AC135438 AC135438	41.6 81.6 241629 2 AC097388 41.6 81.6 241726 2 AC097121 41.6 81.6 241891 2 AC192675 41.6 81.6 24389 2 AC120850 41.6 81.6 24366 2 AC113313 41.6 81.6 244366 2 AC113313 41.6 81.6 244366 2 AC113313 41.6 81.6 244388 2 AC122065 41.6 81.6 244388 2 AC122065 41.6 81.6 244388 2 AC123065 41.6 81.6 244389 2 AC123065 41.6 81.6 24780 2 AC108663 41.6 81.6 24780 2 AC108663 41.6 81.6 24780 2 AC11320 41.6 81.6 24780 2 AC108663 41.6 81.6 24780 2 AC11370 41.6 81.6 24786 2 AC11370 41.6 81.6 24780 2 AC108663 41.6 81.6 24780 2 AC11370 41.6 81.6 248458 2 AC11577

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Alpha-2 adrenergic receptor polymorphisms
Patent: WO 0179561-A 1 25-OCT-2001;
Liggett, Stephen B. (US); Small, Kersten
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Kutsenko,A.S., Gizatullin,R.Z., Al-Amin,A.N., Wang,F., Kyasha,S.M., Podowski,R.M., Muravenko,O.V., Podowski,R.M., Matushkin,Y.G., Gyanchandani,A., Muravenko,O.V., Leviteky,V.G., Kolchanov,N.A., Protopopov,A.I., Kashuba,V.I., Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R. Kisselev,L.L., Wasserman,W., Wahlestedt,C. and Zabarovsky,E.R.
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                                                                                                                                                                                                    Lomasney, J.W., Lorenz, W., Allen, L.F., King, K., Regan, J.W., Yang-Feng, T.L., Caron, M.G. and Lefkowitz, R.J.
Expansion of the alpha 2-adrenergic receptor subtype, characterization of a human alpha 2-adrenergic receptor subtype, the gene for which is located on chromosome 2
Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 2072)
Au-Young, J. and Seilhamer, J. J.
Composition for the detection of signaling
Patent: US 6500938 A 1181 31-DEC-2002;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                                                             Original source text: Human placenta Draft entry and computer-readable sec by J.W.Lomasney, 03-WAY-1990, for rel
                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                  alpha-2-adrenergic receptor; plasma membrane receptor-coupled G protein.
                                                                                                                                                                                                                                                                                                                                                                                               M34041.1 GI:178197
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ilarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
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413. .1765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="unknown"
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                              .1765
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0.0016;
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s sequence :
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e for [1] kindly a
                                                                                                                                after publication
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Paris,H.

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Query Match

100.0%; Score 51; DB 6; Length 3274;
Best Local Similarity 100.0%; Pred. No. 0.0016;

Matches 51; Conservative 0; Mismatches 0; Indels
                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                             Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                     Homo sapiens alpha2B-adrenergic complete cds.
AF005900
                                                                                                                                                                                                                                                                                                                          Patent: WO 02061087-A 41 08-AUG-2002;
Lifespan Biosciences, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigenic peptides
Patent: WO 0206108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burmer,G.C., Roush,C.L. and Brown,J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying su
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 41 from Patent
AX548756
AX548756.1 GI:25813686
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/_ame 'ADRA2RL1'"
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Pred. No. 0.0016;
'; Mismatches 0;
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receptor (alpha2C2AR)
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VERSION
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AL662790
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TITLE
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COMMENT
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AUTHORS
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AUTHORS
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Direct Submission
Submitted (26-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                            sequence.
AL662790
AL662790.21
                                                                                                                                                                                                                                                                 AL662790
Mouse DNA
                                                                                                Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (bases 1 to 133405)
                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHU Rangueil, Toulouse 31403, France
Sequence update by submitter
On Aug 5, 2003 this sequence version replaced gi:2245627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-AUG-2003) INSERM Unit 317, Institut Louis Bugnard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cayla,C., Heinonen,P., Viikari,L., Schaak,S., Snapir,A.
Bouloumie,A., Karvonen,M., Pesonen,U., Scheinin,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (29-MAY-1997) INSERM Unit 317, Institut Louis Bugnard,
CHU Ranqueil, Toulouse 31403, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 9944)
Cayla, C., Schaak, S., Bouloumie, A., Devedjian, J.C. and Paris, H.
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Cayla,C., Heinonen,P., Viikari,L., Schaak,S., Snapir,A.,
Bouloumie,A., Karvonen,M., Pesonen,U., Scheinin,M. and Paris,H.
Alpha2C2-adrenergic receptor gene
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                              ilarity 100.0%; E
Conservative 0;
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sequence from clone RP23-53E2 on
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'note="alpha2C2 adrenergic
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Gene="alpha2C2AR"
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Pred. No. 0.0015;
Mismatches 0
                                                                                                        Craniata; Vertebrata; ;
Sciurognathi; Muridae;
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                                                                                                Euteleostomi; 
; Murinae; Mus.
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SOURCE ORGANISM

VERSION KEYWORDS ACCESSION DEFINITION

AF005900.2

RESULT 7 AF005900

AF005900

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ORIGIN

Gaps

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FEATURES

Bource

JOURNAL

REFERENCE AUTHORS TITLE

DEFINITION ACCESSION VERSION KEYWORDS

SOURCE

ORGANISM

RESULT 6 AX548756 LOCUS

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1292

ORIGIN

Chromosome 2.

Query Match Best Local Similarity

Matches

51;

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REFERENCE
AUTHORS
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSENCT: TT. TRAMPL. Who workers to confirm the workers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9337
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus chromosome 11 clone RP23-53B2 map 11, SEQUENCE, 6 unordered pieces.
AC069060
AC069060.4 GI:29029385
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 216444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-53E2 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                            Mus musculus chromosome 11, clone RP23-53E2
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC069060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISSPROT; {\tt Tr:}, {\tt TREMBL}; {\tt wp:}, {\tt WORMPEP}; {\tt Information} on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 29, 2002 this sequence version replaced gi:21955513.
                                                                                                                                                                                                                                                                          Birren, B., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                        (bases 1 to 216444)
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Sciurognathi; Muridae;
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WORKING DRAFT
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Graind-Pietre, M., Grant, G., Haggs, H., HastCord, A., Horton, L., Kateland, J. C., Iliav, I. Johnson, J., Jones, C., Kann, L., Katelas, A., Klain, J., Laboque, K., Lamazares, R., Landers, C., Kann, L., Katelas, A., Klain, J., Laboque, K., Lamazares, R., Landers, T., Laboque, N., Laboque, K., Lamazares, R., Landers, T., Laboque, N., Laboque, N., Laboque, N., Laboque, N., McCanthy, M., McChan, P., McCautk, A., McKarnan, K., McChesters, R., McIdrim, J., Meness, L., Milboya, T., Mradiad, C., Manga, V., Morrow, J., Will, N., McKarnan, K., McChesters, R., McIdrim, J., Manderson, S., Candour, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T., M., Olivar, T., M., O'Connor, T., O'Donnell, P., Royov, P., Rohman, D., Stanger, T., Tarana, J., Tarana, K., Sericas, M., Standerson, S., Thodoxor, J., Tirrell, N., Travers, M., Trigillo, J., Voung, G., Zainoun, J., Zimmer, A. and Zody, M. X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M. X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M. X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M. X., Wyman, D., Ye, W. J., Thirty, J., Dones, C., Lander, B., Nabaum, C., Lander, B., Corm, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fro., S., Ferreira, P., Fitzeerald, M., Gage, D., Galagan, J., Gardyna, S., Grahan, L., Gard, H., Kalins, W., Iliev, J., Johnson, E., Jones, C., Kalins, J., Kalins, W., Liev, J., Johnson, E., Johnson, E., Johnson, J., Kalins, W., Liev, J., Johnson, E., Johnson, J., Kalins, W., Liev, J., Johnson, R., Washill, C., Lander, T., Levine, R., Ecc., Rogov, P., Roman, J., Kalins, W., Liev, J., Johnson, S., Schaper, B., Wall, J., Kalins, W., Liev, J., Johnson, S., Schaper, P., Saith, C., Span, J., Kalins, W., Liev, J., Johnson, S., Schaper, P., Saith, C., Span, J., Kalins, W., Liev, J., Johnson, S., Schaper, P., Smith, C., Span, J., Kalins, W., Liev, J., Johnson, S., Schaper, P., Smith, C., Span, J., Kalins, J., Kalins, W., Johnson, J., Schaper, J
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<sup>\*</sup> NOTE: This is a 'working draft' sequence. It currently

\* consists of 6 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

1 12827: contig of 12827 bp in length

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REFERENCE
AUTHORS
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AUTHORS
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ASP427259
LOCUS
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Matches 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 92.0
               Douzery,E.J.P., Delsuc,F., Stanhope,M.J. and Huchon,D.
Local molecular clocks in three nuclear genes: divergence times for
rodents and other mammals, and incompatibility among fossil
       J. Mol.
                                                                                                   Huchon,D., Madsen,O., Sibbald,M.J., Ament,K., Stanhope,M.J., Catzeflis,F., de Jong,W.W. and Douzery,E.J.
Rodent phylogeny and a timescale for the evolution of Glires: evidence from an extensive taxon sampling using three nuclear genes Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
                                                                                                                                                                                        Anomalurus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Anomaluridae;
                                                                                                                                                                                                                                                 AJ427259.1 GI:21655549
A2AB gene; alpha 2B adrenergic receptor.
Anomalurus sp.
                                                                                            2082125
                                                                                                                                                                                                                                                                                                                          exon 1
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clone_end:T7
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16683: contig of 3756 bp in length
16783: gap of 100 bp
25277: contig of 8494 bp in length
25377: gap of 100 bp
40696: contig of 15319 bp in length
40796: gap of 100 bp
138890: contig of 98094 bp in length
13890: gap of 100 bp
216444: contig of 77454 bp in length
(2003) In press
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lone_lib="RPCI-23 Female Mouse
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92.0%;
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Pred. No. 0.088;
0; Mismatches
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                                 Madsen, O.
Direct Su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (16-DEC-1997) O. Madsen,
Department of Biochemistry, PO Box
                                                                                                                                                                                                                                                                   alpha adrenergic receptor; subtype 2B.
Oryctolagus cuniculus (rabbit)
Oryctolagus cuniculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
                                                           Revised by [3]
3 (bases 1 to 1183)
                                                                                            NETHERLANDS
                                                                                                                                                          Madsen, O.
                                                                                                                                                                                                  Highly congruent molecular support of edemic African mammals
                                                                                                                                                                                                                                Stanhope, M.J., Madsen, O., Waddell, V.G., and Springer, M.S.
                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus gene encoding alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y15946.2 GI:6448590
                                                                                                                                                                                                                                                                                                                                                                                                  subtype 2B, partial.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (04-JAN-2002) Douzery E.J.P., Institut des Sciences d'Evolution, Lab. Paleonto., Paleobio., Phylogenie, Universite Montpellier II, Pl. E. Bataillon, 34 095 Montpellier Cedex 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (bases 1 to 1185)
Douzery, E.J.P.
          Submission
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RALEYNSKRIPRRIKRILLIVVLARANISLEPLIYKEDGGPQPRGREPQCKLAVQEAWYI
AKVPTLSSPLSSAGEANGHPKPPGEKEDGETPEDFGRARALESSWALPINGGQCKKCA
CGASAEEEAEEEEEEEEEEEEPQAVPVSFASVCSQPLQQPQGSRVLATLRGQVLLGR
HVGTTAGGQWWRRRAQLSREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPQCHCKVPH
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|mol_type="genomic DNA"
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97.8%;
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Pred. No. 0.14;
0; Mismatches 1;
 O. Madsen, University
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                                                                                            University of Nijmegen,
9101, NL-6500 HB Nijmegen,
                                                                                                                                                                                                        for a diverse superordinal clade
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of Nijmegen,
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                                                                                                                                                                                                                                                                                                                                                                                 Madsen, O.O.M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Highly congruent molecular support for a diverse superordinal clade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Springer, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stanhope, M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (rabbit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha adrenergic receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subtype 2B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryctolagus
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On Nov 17, 1999 this sequence
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/product="alpha adrenergic receptor subtype 2B"
/protein_id="CAA75115.1"
/protein_id="CAA75115.1"
/db_xref="GO1:3288562"
/db_xref="GOA:077830"
/db_xref="SWISS-PROT:077830"
/db_xref="SWISS-PROT:077830"
/db_xref="SWISS-PROT:077830"
/db_xref="SWISS-PROT:077830"
/db_xref="SWISS-PROT:077830"
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DILVATLIIPFSLANELLGYWYERRTWXXVYLALDVLFCTSSIVHLCAISLDRYXAVS
RALEYNXKRTPRRIKCIILTVWLIAAAISLPPLIYKGDQGPQPHGAPQCKLNQEAWYI
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DILVATLIIPFSLANELLGYMYERTWCEVYLALDVLFCTSSIVHLCAISLDRYWAVS
RALEYMCKRTPRRIKCIILTVWLIAAAISLPPLIYKGDOGPOPHGAPOCKLNOBAWYI
LSSLGSFFVPCLIMILVYLRIYLIAAAISLPFLKGGPFEGGESQAOCKEGV
KKLPTLATPVASASEANGPSKPAGEKEBGETPBDFGTOALPPGWATLPNSGQGGKEGV
SGASLEEEAEEEEEEEEEEEEPQAVPVSPASVGSPPLQOPOGSRVLATLRGQVLVGRG
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/protein_id="CAA75899.2"
/db_xref="GI:6448591"
                                                                                                                                                                                                                                   /organism="Oryctolagus
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                       Madsen, University of Nijmegen, Box 9101, NL-6500 HB Nijmegen,
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Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreita, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Meneus, L., Mihova, T., Meneus, L., Mihova, T., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phinkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus clone RP23-59D8,
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Birren,B., Nusbaum,C.
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LF"
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COMMENT

http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research

Center clone name: 59\_D Center project name:

-- Summary Statistics

Contact: sequence\_submissions@genome.wi.mit.edu

Web site: http://www-seq.wi.mit.edu

On Oct 22, 2002 this sequence version replaced gi:20336084.

Ri repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://frp.geograf. Submitted (22-OCT-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

JOURNAL

Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

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Gaps
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REFERENCE AUTHORS KEYWORDS SOURCE RESULT 14 AC103291 ACCESSION VERSION DEFINITION B ORIGIN ORGANISM Matches Query Match Best Local Bryant, N. Buhay, C., Burch, P., Burch, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Cessar, H., Center, A.,
Cleveland, C., Chen, G., Chen, R., Chen, Y., Chen, Z.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D., Souza, I.,
Davis, M. D., Davis, C., Day, Carroll, L., De Anda, C., Dederich, D.,
Davis, M. D., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Maheshwari, M., Mahindarene, M., Mahmoud, M., Malloy, K., Mangum, B., Mapua, P., Martin, K., Martin, R., Martin, E., Martin, R., Martinez, E.,
Milosavlievic, A., Miner, G., Minia, R., Monremavor, T.,
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Marchan, E., Martin, R., Marti misc\_feature Local Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Be
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Muzny, D. Marie Rattus norvegicus Eukaryota; Metazoa; HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP Rattus norvegicus (Norway rat) Rattus AC103291 215065 bp DNA linear HTG 09-N Rattus norvegicus clone CH230-13104, WORKING DRAFT SEQUENCE, AC103291.5 GI:24819202 1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAAGAG 48 45; Similarity (bases 1 to 215065) Conservative Allen, Metzker, M. Lee., Abramzon, S., Allen, H., Alsbrooks, S., Amin, A., A. Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Adams, C., Alder, J., ,M., Benahmed,F., HTG 09-NOV-2002

Sequencing vector: Plasmid; n/a; 100% of reads chemistry; Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 204584 bases at least Q40 Consensus quality: 205483 bases at least Q30 Insert size: 20500; agarcse-fp Insert size: 20500; sum-of-contigs Quality coverage: 10.1 in Q20 bases; sgarcse-fp Quality coverage: 10.1 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

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FEATURES
      misc_feature
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1 30760: contig of 30760 bp in length
30861: 30860: gap of 100 bp
30861: 31511: contig of 651 bp in length
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30861
31512
31612
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91260: contig of 41176 bp in length
91360: gap of 100 bp
91360: contig of 13395 bp in length
111714: contig of 20354 bp in length
111814: gap of 100 bp
134604: contig of 22690 bp in length
134604: gap of 100 bp
134604: gap of 100 bp
165128: contig of 30524 bp in length
165128: contig of 30524 bp in length
165128: gap of 100 bp
197581: contig of 3233 bp in length
206933: contig of 3252 bp in length
206933: contig of 3252 bp in length
                                        .31511
                                                                                                                                                                                                                                                             Qualifiers
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gap of 100 bp
contig of 4878
gap of 100 bp
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Milosavljevic, A., Miner, G., Minja, E., Morgan, M., Morris, K., Morris, S., Munic

Montemayor, J., Moore, S., dasa, M., Murphy, M., Nair, L.,

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Pateriak, S., Okwionu, G., Olampunsagoon, A., Pell, S., Parks, K., Pateriak, S., Pall, H., Perez, A., Perez, L., Perez, L
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REFERENCE AUTHORS TITLE

TITLE JOURNAL

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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC112440 222507 bp DNA lin
Rattus norvegicus clone CH230-144K15, WORKING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 84.7%;
Similarity 93.8%;
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202478. .203219
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:lone_end:Sp6"
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/note="clone_boundary
clone_end:T7
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/db_xref="taxon:10116"
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Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,

data.html).

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AL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One On Nov 15, 2002 this sequence version replaced gi:22856702. The sequence in this assembly is a combination of BAC based reads (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
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                                                                                        Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Conter Project Information
Center project name: GRYP
Center clone name: CH230-144K15
Assembly program: Phrap; version 0.990329
Consensus quality: 20632 bases at least Q40
Consensus quality: 208648 bases at least Q30
Consensus quality: 209801 bases at least Q20
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Best Local Similarity
RS Muzny, D.Mazie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiano, D., Balder, J., Anguiano, D., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, L., Ceastar, H., Center, A., Clacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Deckrell, R., Cox, C., Coyle, M., Cree, A., D., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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Rattus norvegicus (Norway rat)
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Rattus norvegicus clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53078
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57499. .58533
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109071. .110316
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62821. .64890
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|mol_type="genomic DNA"
|db_xref="teaxon:10116"
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93.8%; Pred. No. 0.11;
7ative 0; Mismatches 3;
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1e CH230-236K3, WORKING DRAFT SEQUENCE,
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Gaps

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REFERENCE AUTHORS

JOURNAL

Direct Submission

Rat Genome Sequencing Consortium.

REFERENCE AUTHORS TITLE

JOURNAL

Direct Submission Worley, K.C. Unpublished

(bases 1 to 222507)

Submission

COMMENT

Center code: BCM Web site: http://

Center: Baylor College of Medicine

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Gracer, C. M., Gobisi, A., Gonta, R., Gaccis, A., Garnar, T., Gazza, M., Gurrar, M., Handland, M., Handland, M., Harnandez, M., Hernandez, R., Hilves, S., Hladun, S.L., Handardor, M., Hernandez, M., Hernandez, R., Hilves, S., Hladun, S.L., Handardor, M., Hernandez, M., Hernandez, R., Hilves, S., Hladun, S.L., Handardor, M., Hongan, M., Jackson, L., Jang, H., Kang, L., Kovar, C., Litt, J., Litt, J.,
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Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,
Anyal-bechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranake, D., Barber, M., Barnstead, M., Benahmed, F.,
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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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Rattus norvegicus clone CH230-21B17,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="wgs_contig"
224751. .226214
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1975. .3636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="wgs_contig"
221697. .223335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="wgs_contig"
3737. .4954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="CH230-236K3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.7%;
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7, *** SEQUENCING
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IN PROGRESS
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AL Submitted (23.NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

The sequence in this sequence version replaced gi:23321740.

and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig described individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ms to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gebregoorgis, B., Geer, K., Gill, R., Garcia, A., Garner, T., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hollins, B., Howells, S., Hladun, S.L., Hodgson, A., Hogues, M., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, B., Johnson, R., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Liu, J., Liu, J., Liu, J., Lorensuhwa, L., Loulesged, H., Lorgacre, S., Lopez, J., Liu, J., Mahsehwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Martin, R., Martin, R., Martin, R., Martinez, B., Mayan, P., Martin, K., Martin, R., Martinez, B., Makelmen, S., McLeod, M.P., McKeill, T.Z., Mennen, E., Morgan, M., Morris, K., Morris, S., Munidaas, M., Murphy, M., Nair, L., Pasternak, S., Paul, H., Perez, A., Perez, L., Fannkoch, C., Puazo, M., Oarmbunsegon, A., Richer, S., Reyes, K., Popper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L., L., Retlly, B., Reves, K., Regier, M., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Shetty, J., Shwartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shatsman, S., Shen, H., Steen, S., Soott, G., Shatsman, S., Shen, H., Sheed, A., Sodergren, E., Song, Z., Stotter, S., Sotter, C., Smajs, D., Wang, A., Sisson, I., Sitter, C.D., Smajs, D., Shatsman, S., Shen, H., Sheed, A., Sodergren, E., Song, Z., Stotter, C.D., Smajs, D., Walte, R., Wang, O., Wang, S., Wutten, A., Steek, A., Tabor, P., Taylor, C., Wang, O., Wang, S., Wutten, A., Steek, A., Tabor, P., Taylor, C., Wang, O., Warren, J., Warren, R., Walker, B., Wang, J., Zhou, J., Yakub, S., Yen, J., Wang, D., Wang, J., Zhou, J., Yakub, S., Yen, J., Woon, L., Yoon, L., Wang, J., Zhou, J., Shath, D., Wang, J., Wang, J., Panks, R., Smith, D., R., J., Smith, D., R., J., Smith, J., Smith, J., On, J., Smith, H.O., J., Smith, J., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Direct Submission
                                                                                                                                       Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc.help@bcm.tmc.edu
Center project Information
Center project name: CH230-21817
                                                                Assembly program: Phrap; versior Consensus quality: 256550 bases
                                                                                                                                                                                                                                                                                                         lenter: Baylor College of Medicine
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                                                          version 0.990329
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Best Local
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AC095903.9 GI:24940776
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                                                             Rattus norvegicus clone CH230-10L19,
***, 5 unordered pieces.
AC095002
                                                                                                                             AC095903
                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a "working draft" sequence. It currently
consists of 11 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence in as soon as it is available and the accession number will be preserved.
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281734
283732
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276816
278213
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280003
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97148
101762
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254652
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Consensus quality: 263748 bases at least Q30
Estimated insert size: 265322; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="wgs_contig"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wg8_contig"
254752. .255877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_contig"
258325. .259516
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101862. .103060
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/clone="CH230-21B17"
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101761: contig of 4614 bp in length
101861: gap of unknown length
254651: contig of 152790 bp in length
254551: gap of unknown length
25424: contig of 373 bp in length
258224: contig of 3473 bp in length
271487: contig of 3133 bp in length
271487: contig of 31183 bp in length
276715: contig of 1183 bp in length
377615: contig of 1528 bp in length
476815: gap of unknown length
576815: gap of unknown length
576815: gap of unknown length
576815: gap of unknown length
587812: contig of 1528 bp in length
587812: contig of 1528 bp in length
587812: contig of 1528 bp in length
587812: contig of 1537 bp in length
587812: gap of unknown length
588012: gap of unknown length
588012: gap of unknown length
588012: gap of unknown length
588013: gap of unknown length
588031: gap of unknown length
588731: contig of 1531 bp in length
588731: contig of 1938 bp in length
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                    84.7%; Score 43.2; DB 2;
93.8%; Pred. No. 0.11;
ative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .287497
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.258224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .98506
                                                                DNA linear
9, *** SEQUENCING
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REFERENCE AUTHORS TITLE JOURNAL

REFERENCE AUTHORS TITLE JOURNAL

Unpublished 2 (bases 1

COMMENT

Center:

Length 287497; Indels

o,

Gaps

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TITLE
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                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Allen, C., Allen, M., Beroks, S., Manin, A., Ragilano, D., Allen, V., Anyalebechi, V., Aoyaeji, A., Ayodeji, M., Baca, E., Baden, H., Anyalebechi, V., Bandaranaike, D., Barber, M., Barnistead, M., Benahmed, F., Biawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Chu, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cheveland, C., Coyle, M., Cree, A., D'Souza, L., Delyado, O., Denson, S., Dermo, G., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bayene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Golevara, W., Ganrar, T., Garza, M., Gebregeovgis, E., Geer, K., Gill, R., Grady, M., Guerer, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Durch, K., Warten, P., Harland, B., Hadden, S.L., Hodgson, N., Hermandez, M., Hernandez, R., Hines, S., Haldun, S.L., Hodgson, N., Heryes, M., Harvay, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, M., Hernandez, R., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J., Liu, Y., Loudon, P., Longacre, S., Lopez, J., Liu, J.,
                                Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 13, 2002 this sequence version replaced gi:22772685. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                              of Molecular and Human Genetics,
Baylor Plaza, Houston, TX 77030,
3 (bases 1 to 293183)
                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing
Submitted (17-SEP-2001) Human Genetics, Baylor College
                                                                                                                                                                                                                                                     Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
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Nov 13, 2002 this sequence version replaced gi:22772685.
e sequence in this assembly is a combination of BAC based reads
d whole genome shotgun sequencing reads assembled using Atlas
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                                                                                                                                                                                                                                              Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                   Center, Department of Medicine, One
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(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
                                                                                                contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
table.
                                     shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                           and separated
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FEATURES
                                                                                                                                                                           misc_feature
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                                                   misc_feature
                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                               misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: GDVC
Center clone name: CH230-10119
Center clone name: CH230-10119
Center clone name: CH230-10119
Center Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 227421 bases at least Q30
Consensus quality: 229231 bases at least Q30
Consensus quality: 239603 bases at least Q30
Consensus quality: 230603 bases at least Q30
Estimated insert size: 234846; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48443
289478
289578
291427
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----- Project Information
Center project name: GDVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
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44442
48343
                                                                                                                                                                                                                                                                                                                                                              9810. .10659
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clone_end:T7
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clone_end:Sp6"
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231098. .232521
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181343. .182203
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48443. .51434
                                                                                                                                                                                                                                                                                       44442.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="CH230-10L19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44441: gap of unknown length
48342: contig of 3901 bp in length
48442: gap of unknown length
289477: contig of 241035 bp in length
289577: gap of unknown length
291426: contig of 1849 bp in length
291526: gap of unknown length
293183: contig of 1657 bp in length.
                                                                                                                                                                                                                                                                                                             sequence:BH307090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44341: contig of 44341 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Center
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ORIGIN

Query Match
Best Local Similarity
Matches 45; Conserv

Conservative

0

Score 43.2; DB Pred. No. 0.11; 0; Mismatches

BB N -: ω --

Length 293183; Indels

0;

Gaps

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84.7%; 93.8%;

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ORIGIN
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Best Local S
Matches 46
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                                                                1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAAGAGTGT 51
                                                                                                                                                                              46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (04-JAN-2002) Douzery E.J.P., Institut des Sciences d'Evolution, Lab. Paleonto., Paleobio., Phylogenie, Universite
Montpellier II, Pl. E. Bataillon, 34 095 Montpellier Cedex 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Douzery, E.J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Douzery,E.J.P., Delsuc,F., Stanhope,M.J. and Huchon,D. Local molecular clocks in three nuclear genes: divergence times rodents and other mammals, and incompatibility among fossil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Huchon, D., Madsen, O., Sibbald, M.J., Ament, K., Stanhope, M.J., Catzeffils, F., de Jong, W.W. and Douzery, E.J.
Rodent phylogeny and a timescale for the evolution of Glires:
evidence from an extensive taxon sampling using three nuclear genes
Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AJ427260.1 GI:2165824
AJ427260.1 GI:2165824
AZAB gene; alpha 2B adrenergic receptor.
Castor canadensis (American beaver)
Castor canadensis (Enerican beaver)
Castor canadensis (Eutharios; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Castoridae; Castor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Mol. Evol. (2003) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Castor canadensis partial A2AB c
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/gene="A2AB"
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                                                                                                                                                                                                                                                                                                                                             SAKVPTLVSSLSSTGEANGHPKPPGEKESGETPEDPGARALTPSWVALPNGQQQKKG
VCGASAEEEPEEEEEEEEECEPQAVPVSPASVCSAPLQQPQGSRVLATLRGQVLL
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LASSIGSFFAPCLIMILVYLRIYLIAGRSNRRGFRKKKGFGFRKKKGSCFYFGRAPA
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/protein_id="CAD20298.1"
/db xrefe"G1:2166825"
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                                                                                                                                          Score 43; DB 10; Length 1191;
Pred. No. 0.17;
0; Mismatches 5; Indels
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gene for alpha 2B adrenergic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Gord, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S., Karatas, A., Karlas, A., Kella, C., LaRocque, K., Lamazares, R., Kanat, A., Karatas, A., Kella, C., LaRocque, K., Lamazares, R., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguen, C., Nicol, R., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Roman, S., Severy, P., Senman, S., Severy, P., Senmas, S., Stauge-Thomann, N., Subramanian, A., Tayas, R., Stauge-Thomann, N., Stolyabovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wynan, D., Yesseliev, H., Vo, L., Mison, B., Wu, X., Wynan, D., Yesseliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wynan, D., Yesseliev, H., Sanbos, R., Schauback, R., Stauge-Thomann, N., Stolyabovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wynan, D., Ye, W.J., Young, G., Direct Submission
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                          Submitted (22-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Feb 22, 2003 this sequence version replaced gi:28412068.
                                   All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 217323)
Birren,B., Nusbaum,C. and Land
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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217323 bp DNA
Mus musculus clone RP23-20L18, WORKING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (22-MAR-2002) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA 1 to 217323)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Lander, E.
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Sciurognathi; Muridae; Murinae; Mus.
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Best Local Similarity
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                                             1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118666
118766
120860
120960
123538
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131558
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                                                                                                                                           Conservative
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118766. ...
                                                                                                                                                                                                                                                             vector_side:right"
                                                                                                                                                                                                                                                                                                                                           210473.
                                                                                                                                                                                                                                                                                                                                                                                         /note="a88embly_fragment"
131658. .210372
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
123638. .131557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location,
                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment"
120960. .123537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                          note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="RP23-20L18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118665: contig of 118665 bp in length
118765: gap of 100 bp
120859: contig of 2094 bp in length
120959: gap of 100 bp
123537: contig of 2578 bp in length
123637: gap of 100 bp
131557: contig of 7920 bp in length
131657: gap of 100 bp
210372: contig of 78715 bp in length
210472: gap of 100 bp
210373: contig of 6851 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="taxon:10090"
                                                                                                                                                                  83.5%;
91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end:SP6
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                                                                                                                                           0
                                                                                                                                                                  Score 42.6; DB Pred. No. 0.16;
                                                                                                                                             Mismatches
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                                                                                                                                           4.
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AUTHORS
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                                                                                                                                                                                                                            CE 3 (bases to 232202)

RS Birren, B., Nusbaum, C., Lander, E., Nobelleil, A., Allen, N., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavki, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., MacCarthy, M., MacConald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., MacLind, R., MacLean, C., Noguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasemy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Direct, Submission
                                                            On Dec 15, 2003 this sequence version replaced gi:28927750. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                  Submitted (15-DEC-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                  Direct Submission
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Center: Whitehead
Center code: WIBR
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Institute/ MIT Center for Genome Research

ORIGIN

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Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Garaham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauser, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 232202)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC115740.4 GI:39841512
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
Mus_musculus (house mouse)
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                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Coll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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me 3, clone RP23-476G18
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e 3 clone RP23-476G18 map 3,
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Wellcome Trust Sanger Institute Center code; SC Web site: http://www.sanger.ac.uk
                                                                                                    Submitted (02-UIL-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirtes: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Sequence from the Mouse Genome Sequencing Consortium whole genome Sequencing Consortium whole genome shotgun alone has only been used where it has phred quality of at least 30.
During sequence assembly data is compared from overlapping clones.
                                                   Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                          Chapman,
                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                      BX465209.7 GI:32439584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse DNA sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX465209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAGT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                   Submission
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143697
148480
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Center project name: L22818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48580
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72078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                            ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone="RP23-476G18"
'clone_lib="RPCI-23 Female Mouse BAC"
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mol_type="genomic DNA"
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chromosome="3"
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143596: contig of 71519 bp in length
143696: gap of 100 bp
148479: contig of 4783 bp in length
148479: contig of 4783 bp in length
200240: contig of 51661 bp in length
123202: contig of 51661 bp in length
1 23202: contig of 51662 bp in length
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91.8%;
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Pred. No. 0.16;
0; Mismatches 4;
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m clone RP23-359C20 on chromosome X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 232202;
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                                                                                                                                                         Sequence data
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AUTHORS
TITLE:
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AL672046/c
                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
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Matches

FEATURES

RESULT 22

REFERENCE AUTHORS TITLE

JOURNAL

SOURCE CEYWORDS VERSION ACCESSION DEFINITION BX465209/c

ORGANISM

COMMENT

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Query Match
          AL Submitted (21-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:

On May 16, 2002 this sequence version replaced gi:20339178.

On May 16, 2002 this sequence version replaced gi:20339178.

Where difference assembly data is compared from overlapping clones. together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequence with a corresponding to the overlapping clone, as we submit sequence with finished as follows unless otherwise noted: all chemistry or covered by high quality data (i.e., phred quality sequence made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least assembly was confirmed by restriction on M13 subclone; and the assembly was confirmed by restriction dieser the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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This sequence was finished above.

regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality some compressions and repeats; all regions were covered by high quality data (i.e., phred quality some plasmid subclone or more than one M13 subclone; and the ascompressions and repeats; all regions were covered by at least occasion of the clone being a yAC.

The following abbreviations are used to associate primary accession on the Wormper database can be found at from the RPCI-23 Mouse BAC Library—

Normal Subcomper RP23-359C20 is formation of pharer As Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               814
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 186272)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL672046.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186272 bp DNA linear ROD 22-MAY-2002
sequence from clone RP23-299F14 on chromosome X, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GI:20870744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="RP23-359C20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.7%;
93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42.2; DB
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
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following
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FEATURES

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RESULT 24
AC128836
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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Muzny, D. Marie, Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Bader, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Bader, H., Ballen, D., Bandaranaike, D., Barber, M., Barca, E., Bader, H., Baldwin, D., Bandaranaike, D., Barber, M., Barretad, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Davis, G., Davyl-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Delgan, A., Becotto, M., Eugene, C., Evans, G.A., Falls, T., Fan, G., Fraser, C., M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Ghoranathe, P., Hayland, W., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Hernandez, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebbow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Lorensuhewa, L., Louleged, H., Lozado, R.J., Lux, Malloy, K., Mangum, A., Mahndartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mahndartne, M., Mahmoud, M., Malloy, K., Mangum, A., Morris, S., Montemayor, J., Moore, S., Milosa, M., Morris, S., Montemayor, J., Moore, S., Montemayor, J., Morris, S., Montemayor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC128836.3 GI:25139497
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus clone CH230-485K2, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-299F14 is from the RPCI-23 Mouse PAC Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMEL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unordered pieces
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/db_xref="taxon:10090"
/chromosome="X"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RP23-299F14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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93.6%;
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Pred. No. 0.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189624 bp
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KEYWORDS ACCESSION

REFERENCE

AUTHORS

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AL Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:22855866.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hggc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L., Pluzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reeter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Sovergren, B., Song, X.-Z., Sorelle, R., Sosa, J., Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Sosa, J., Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Sosa, J., Shen, H., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Walder, B., Wang, J., Warren, J., Waldron, L., Walker, B., Wang, J., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Wang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat Genome Sequencing Consortium.
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3 (bases 1 to 189624)
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                                               table.
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    Genome Center
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REFERENCE AUTHORS

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COMMENT

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NOTE: Bstimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This is a 'working draft' sequence. It currently
consists of 7 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project Information
Center project name: CH230-485K2
Center clone name: CH230-485K2
Center summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 178577 bases at least Q40
Consensus quality: 180920 bases at least Q40
Consensus quality: 182691 bases at least Q20
Consensus quality: 182691 bases at least Q20
Bstimated insert size: 183435; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Baylor College of Medicine Center code: BCM
        8264
8263: contig of 8263 bp in length 8363: gap of unknown length
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REFERENCE
AUTHORS
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KEYWORDS
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AC128202/c
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RS Muzny D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Brant, N., Bullay, C., Burch, P., Burrell, K., Calderon, E., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chen, C., Coyle, M., Cree, A., D'Souza, L., Cox, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Egan, A., Escotto, M., Elgen, C., Evans, C.A., Falls, T., Fan, G., Faraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hermandez, J., Hermandez, R., Hadun, S.L., Hodgson, A., Hogues, M., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., Khan, Z., King, L., Kovar, C., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Mahenshwari, M., Mahindartne, M., Mahmoud, M., Martin, R., Martinez, E., Milosavlievic, A., Miner, G., Minia, B., Montemavor, J., Mont
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAAGA 47
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norvegicus clone CH230-423P19, *** SEQUENCING
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35358. .37673
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|mol_type="genomic DNA"
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112776: contig of 77419 bp in length
112876: gap of unknown length
16816: contig of 53940 bp in length
166916: gap of unknown length
166916: gap of unknown length
166916: gap of unknown length
166995: contig of 2079 bp in length
17130: contig of 2635 bp in length
17130: gap of unknown length
17130: gap of unknown length
171830: gap of unknown length
188624: contig of 17794 bp in length.
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93.6%;
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Pred. No. 0.2;
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Direct Submission

AL Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 7030, USA

On Nov 20, 2002 this sequence version replaced gi:23908157.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baylor Plaza, Houston, TX 77030, t
3 (bases 1 to 189886)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 189886)
Worley, K.C.
Direct Submission
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center clone name: CH230-423919
Center clone name: CH230-423919
Assembly program: Phrap; version 0.990329
Consensus quality: 175673 bases at least Q40
Consensus quality: 175673 bases at least Q30
Consensus quality: 17988 bases at least Q30
Consensus quality: 17900 bases at least Q30
Estimated insert size: 177946; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. \* NOTE: Estimated insert size may differ from sequence length
\* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).

\* NOTE: This is a 'working draft' sequence. It currently
\* consists of 2 contigs. The true order of the pieces
\* is not known and their order in this sequence record is

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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                    SOURCE
ORGANISM
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VERSION
KEYWORDS
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AL691481
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Best Local Similarity
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                                                                                                                                       Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                  AL691481 230127 bp DNA linear ROD 26-MAR-2003 Mouse DNA sequence from clone RP23-173C3 on chromosome 4 Contains a muscle enclase 3 beta (Enc3) pseudogene, a mitochondrial H+ transporting ATP synthase FO complex subunit d (Atp5h) pseudogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 230127)
                                                                                                                                                                                                                                                                                                                                                                     AL691481.15 GI:22213670
HTG; Atp5h; CpG island; Eno3.
                                                                                                                                                                                                                                                                                                                                                                                       AL691481
AL691481.15
                                                    During sequence assembly data is compared from overlapping clones
                                                                                                         Web site: http://mrcseq.har.mrc.ac.uk
                                                                                                                             Center code:
                                                                                                                                                                                                                           Submitted (17-MAR-2003) Wellcome Trust Sanger Institute, Hinxton
                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                        Contact: mouseq@har.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                         CpG island,
                                                                                                                                                                                                                                                  Submission
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clone_end:Sp6"_
182895. .184020
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/note="clone_boundary
clone_end:Sp6
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clone_end:Sp6"
187014. 188573
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complement(4656. .4851)
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clone_end:Sp6"
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clone end:T7"
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'clone="CH230-423P19"
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mol_type="genomic DNA"
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                                                                                                                             UK-MRC
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93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       complete sequence.
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Pred. No. 0.
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replaced gi:21748253.
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Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was finished as follows unless otherwise noted: all regions were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is the entire insert of clone RP23-173C3 The true left end of clone RP23-426J14 is at 226462 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence day from the whole genome shotgun alone has only been used where it his a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

RP23-173C3 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.

For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VECTOR: pBACe3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1183. .1193
/note="2.2 c
                          /note="L2 repeat: matches 2228. .2955 of consensus"
6700. .6713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1 repeat: matches 3932. .5048 of consensus" complement(2570. .2768)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1268. .1295

/note="28.0 copies 1 mer T 20% conserved"

complement (1344. .2415)

/mplement (1344. .2415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="26.0 copies 2 mer TG 86% conserved"
complement(956. .1118)
/note="B3A repeat: matches 8. .178 of consensus"
                                                                              complement (5128.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              898. .949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="3.0 (
1260. .1275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="ll repeat: matches 4623. .4828 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="4.0 copies 4 mer TTTC 23% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="4.5 copies 4 mer TTTA 29% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="match: GSS: Em:AZ561521"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="RP23-173C3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .230127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 695
                                                                                                                                                                                           .=.5.0 copies 2 mer
                                                                                    .0 copies 5 mer
nt(5128. .5791)
                                                                                                                                                                   .4 copies 5 mer AAATG 24% conserved'
                                                                                                                                                                                                                                                                             .9 copies 12
                                                                                                                                                                                                                                                                                                                                                                                            .5 copies 6 mer TTTGAT 21% conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                .4 copies 5 mer TACTA 24% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .6 copies 5 mer TTTTC 34% conserved"
                                                                                                                                                                                                                                                                                                                                       .2 copies 5 mer AGGAA 22% conserved"
copies 7 mer ATCATTC 28% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   copies 9 mer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                copies 5 mer TTATT
                                                                                                                                                                                                                                                                                mer AGAAAGAGACAG 49% conserved"
                                                                                                                                                                                                                           გ
G
                                                                                                            AGTGA 21% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTTCTTT 38% conserved"
                                                                                                                                                                                                                           20% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                data
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/nore="1x9 repeat: matches 6857. .7165 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="2.2 copies 5 mer TATTT 22% conserved"
complement (13323 ...13477)
/note="Lx9 repeat: matches 7477. .7644 of consensus"
                                                                                                                                                                                                                                                                                                                                      /note="Lx9 repeat: matches 7125. .7451 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="2.0 copies 21 mer TGGTTAAAAATTGAAACTATT 59%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="13.2 copies 5 mer AAAAG 57% conserved"
11943. .11965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          match: proteins: Sw:P25704 Sw:P15429 Tr:BAB22137
Tr:AAH13460 Sw:P13929 Sw:P21550 Sw:P51913 Tr:AAH24644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="bM173C3.1 (enolase 3, beta muscle (Eno3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MIR repeat: matches 15. .261 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORRIA2 repeat; matches 1. .327 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(8845. .8883)
/note="MIR repeat: matches 58. .95 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="2.5 copies 4 mer ATCT 20% conserved" complement (8845. .8883)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5838. .6855
/note="2.0 copies 9 mer ATCATTATT 36% conserved"
7046. .7063
/note="4.5 copies 4 mer TTTA 27% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ="48.5 copies 2 mer TC 52% conserved"
.7519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             copies 6 mer TTCCCC 26% conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _copies 5 mer TGATA 20% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .6972 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 27
AC112634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
MILEN, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Biswalo, K., Blair, J., Blankenburg, K., Barber, M., Barnstead, M., Benahmed, F., Bryant, N., Bahay, C., Burch, P., Burrell, K., Calderon, E., Chacko, J., Carter, K., Cavzos, J., Ceasar, H., Center, A., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Egan, A., Escotto, M., Eugen, C., Evans, C.A., Falls, T., Fan, G., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garrier, T., Garza, M., Harvey, Y., Havlah, W., Hamil, C., Hamilton, C., Hamilton, K., Houlins, B., Howells, S., Hladun, S.L., Hodgson, A., Hogues, M., Jackson, L., Handerson, N., Hernandez, J., Jackson, L., Liu, J., Liu, Y., Lobow, H., Levan, J., Lews, L., Johnson, R., Jolivet, A., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulesged, H., Lozado, R.J., Lu, X., Lu, X.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS PHASE; HTGS DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC112634 230227 bp DNA linear
Rattus norvegicus clone CH230-122C23, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 230227)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Tandem repeat. Forced join. Gap size estimated be approximately 600bp by restriction digest data." /note="Lx8 repeat: matches 6087..6933 of consensus" /note="Lx8 repeat: matches 6087..6933 of consensus" /note="Lx8 repeat: matches 5727..5846 of consensus" /note="Lx8 repeat: matches 5727..5846 of consensus" /note="1.6.0 copies 1 mer T 23% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:25072799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Sequence confirmed by mouse whole genome shotgun supercontig data sequenced by the Mouse Genome Sequencing Consortium, contig 199684, version 2." complement (21025. 22191) /note="LIF repeat: matches 59. .591 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14502. 14710

Inote="L1 MM repeat: matches 6172. .6380 of consensus" complement (15070. .21003)

Inote="L1F repeat: matches 550. .6618 of consensus" 20673. .20758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(14318. .14499)
/note="L1_MM repeat: matches 6407. .6587 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82.7%;
93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42.2; DB 10;
Pred. No. 0.2;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 230127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG 19-NOV-2002
SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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repeat\_region repeat\_region

/note="2.0 co

.12233

copies 6 mer ATCAAA 24% conserved"

/note="23.0 copies 1 mer A 28% conserved"

repeat\_region repeat\_region

11875. .1 /note="2.

/evidence=not\_experimental 11875. .11888

\_copies 6 mer AACACC 28% conserved"

start=1

complement(10509. .11722) /gene="bM173C3.1"

gene="bM173C3.1"

repeat\_region

/note="3.7 copies 3 mer AAC 22% conserved" complement (9891 . .10099)

misc\_feature repeat\_region

note="match: GSS:

Em:AZ639349"

repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region

9973. .9013 note="20.5 copies 2 mer TG 73% conserved"

.0 copies 2 mer CT 36% conserved"

repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region misc\_feature repeat\_region repeat\_region

> /note="16.3 13907. .1392 13860.

11.2 copies 6 mer CTTCTC 71% conserved"

\_copies 3 mer CTC 55% conserved

.13925

/note="9.0 copies 2 mer CT 36% conserved" complement (13947. .14255)

.3 copies 3 mer CTT 38% conserved

/note="25.5 copies 2 mer AC 93% conserved" complement (13548 ...13856)

13292. .j /note="2.

'note="match: GSS: Em:AZ334877" [3292. .13302 /note≈"Lx repeat: matches 5801. 12565. .13254

complement (12315. .13123)

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Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, R., Martinez, E., Mangum, B., McLeod, M.P., McNeill T.Z., Meenen, E., Mallosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Parks, K., Nankervis, C., Poindexter, A., Perez, L., Pfamikoch, C., Plopper, F., Poindexter, A., Perez, L., Primus, E., Pu, L.-L., Plazo, M., Quiroz, J., Rachlin, E., Revees, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Rose, M., Rose, R., Ruiz, S., J., Riggs, F., Rives, G., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., J., Sanders, W., Savety, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Snetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Snetty, J., Svartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneth, P., Sode, Y., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Wera, V., Villasana, D., Walkor, B., Wang, J., Wang, O., Wang, S., Warten, R., Weix, Mitte, F., Wang, O., Wang, S., Walkor, B., Wang, J., Warten, R., Weix, S., Yen, J., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, J., Zhou, J., Zhou, S., Jen, J., Yoon, V., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23265745.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a casifold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                    Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 230227)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley, K.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.) NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 230227)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
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230313 bp DNA linear HTG 20-NOV Rattus norvegicus clone CH230-12B24, WORKING DRAFT SEQUENCE, 3
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 230227: contig of 230227 bp in length.
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.600. .6570
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/mol_type="genomic DNA"
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AL Submitted (20.NOV-2022) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 20, 2002 this sequence version replaced gi:23265453.

The sequence in this assembly is a combination of BAC based reads (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold, by extend beyond the ends of the clone and there may be sequence genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_donors: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                           NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                             Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mamgum, B., Mapua, P., Martin, K., Martin, R., Martinez, B., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACII1391.4 GI:30578964
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unordered pieces
AC111391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAAGAAGAAGA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC111391 268151 bp DNA linear HTG 13-MAY-20
Rattus norvegicus clone CH230-145D10, WORKING DRAFT SEQUENCE, 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 268151)
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228010
229123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     end_sequence: ##312003
224684. 225557
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end_sequence:BH312063"
226357. .227909
/note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_end_extension
clone_end:Sp6"
5195..5864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="clone_boundary clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="CH230-12B24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .23031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82.7%;
93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence:BH312065"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227909: contig of 227909 bp in length 228009: gap of unknown length 229122: contig of 1113 bp in length 22922: gap of unknown length 230313: contig of 1091 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Qualifiers
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Pred. No. 0.2;
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Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Matlioy, K., Mangum, A.,
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Mangum, B., Mapua, P., Martin, K., Martinez, E.,
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Mandiney, S., McLeod, M.P., McNeill, T.Z., Menen, E.,
Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
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Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nankervis, C., Neal, D., Newton, N., Norris, S., Parks, K.,
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Plopper, F., Poindexter, A., Popovic, D., Primus, E., Put, L.L.,
Plopper, F., Poindexter, A., Perez, L., Pfannkoch, C.,
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Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvattsbeyn, A., Siston, I., Sitter, C.D., Smajs, D.,
Snedd, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soas, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, D., Walter, B., Wangs, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Wang, Q., Wang, S., Shan, M., Shan, J., Yoon, V.,
Yu, F., Zhang, J., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinston, A., Shan, S., Smith, D.R., Holt, R.A., Smith, H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23268032.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hernandez, R., Hinés, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Li, Z., Liu, J., Liu, J., Li, Z., Liu, J., Liu, J., Li, Z., Liu, J., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shotgun sequence only table.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yior Plaza, Houston, TX 77030, (bases 1 to 268151)
Genome Service
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 268151)
Center clone name: CH230-145D10
------ Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 249266 bases at least Q40
Consensus quality: 250442 bases at least Q30
Consensus quality: 251941 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor Co
                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: GMEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/
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REFERENCE AUTHORS

TITLE JOURNAL REFERENCE

TITLE

AUTHORS TITLE

JOURNAL

COMMENT

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                            KEYWORDS
                                           VERSION
                                                          ACCESSION
                                                                                   DEFINITION
                                                                                                                                RESULT 30
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Best Local S
  ORGANISM
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                                                                                                                                                                          85465 GAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAGGAAGA 85419
                                                                                                                                                                                                                                  44;
                                                     1198 bp
Equus caballus gene encoding alpha
partial.
Y15945
                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 10 contigs. The true order of the pieces

* is not known and their order in this sequence record is
alpha adrenergic receptor; subtype 28 Equus caballus (horse)
Equus caballus
                                         Y15945.2 GI:6448521
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as soon as in
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258608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Estimated insert size: 260332; sum-of-contigs estimation Quality coverage: 11x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263201
263301
264672
264772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261100
261200
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37382
49157
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                             end sequence:BH297570"
251B13. .253217
/note="wgs end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                      /note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                         clone_end:T7
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35958.
                                                                                                                                                                                                                                                                                                                                   256289. .257316
                                                                                                                                                                                                                                                                                                                                                                                                                                /note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                     183431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="wgs_contig"
183431. .183726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="CH230-145D10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 266487: gap of 
268151: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257416: gap of
258607: contig
                                                                                                                                                                                                                                            82.7%;
93.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264771: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264671: contig of 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263300: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261199: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258707:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _type="genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .37281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of contig
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contig
                                                                                                                                                                                                                                  0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
                                                                                                                                                                                                                                              Score 42.2;
Pred. No. 0.
                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
of 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
of 1052
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unknown length
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                                                                                   adrenergic receptor subtype 2B,
                                                                                                    DNA
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length
bp in length
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3 (bases 1 to 1198)
3 (bases 2 to 1198)
Madsen, O.
Direct Submission
Submitted (15-NOV-1999) O. Madsen, University of Nijmegen,
Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,
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Direct Submission

Submitted (16-DEC-1997) O. Madsen, University of Nijmegen,

Department of Biochemistry, PO Box 9101, NL-6500 HB Nijmegen,

NETHERLANDS
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Highly congruent molecular support for a diverse superordinal clade of edemic African mammals
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(product="alpha adrenergic receptor subtype 2B"
(protein id="CAA75898.2"
(db_xref="GI:6448522"
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|mol_type="genomic DNA"
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Aas52801 Human gln
Aas224013 Human pol
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Aak52886 Human pol
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Aba40003 Human bra
Aba3046 Human pol
Aak14364 Human gen
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Aak131660 Probe #15
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Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR;
                                                                    alpha-2BAR third intracellular loop encoding DNA
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ABC50434
ABQ17445
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ABQ250435
ABL20181
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Aca03141 Lung canc
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                                                                                                              The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) controlled a sample having a polymorphic site, comprising; (a) site comprising nucleotide positions 901-909 of (I), a site comprising nucleotide positions 901-909 of (I), a site comprising complement of; and (b) detecting a polymorphic comprising nucleotide positions 901-909 of (I), a site comprising comprising of (IIV) or a site comprising comprising comprising detecting a polymorphic site comprising (a) (ggggcgggcgg) or (B) (ggggcggcgg) at positions 961-972 of (III). The comprising detecting a disease associated with alpha2A or alpha2C receptor comprising detecting a polymorphic site which correlate to disease as elected from cardiovascular disease, central nervous system disease and combinations of these. In addition, the technique may be used to predict unitividual's response to an alpha2B, alpha2A, or alpha2C combinations of these. In addition, the technique may be used to predict unitividual's response to an alpha2B, alpha2A, or alpha2C combinations of these or alpha2B, alpha2A, or alpha2C combinations of these) by detecting the polymorphic site and correlating practice to a predetermined response (where the response is correlating correlated by detecting the polymorphic site and correlating the phosphorylation or inositol the sequence includes a 9 nucleotide polymorphic site at nucleotides 901.

The sequence includes a 9 nucleotide polymorphic site at nucleotides 901.
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(SMAL/)
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DB; AAM52117.
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/note= "sequence includes a 9 nucleotide polymorphic site
at nucleotides 901-909 absent in the alpha-2BAR variant
(AAI99906)"
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                                                                                                                                                                                                                 Sequence 1353 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Snapir A, I
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GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAAGAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heinonen P, A
Salonen JT,
                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product=
protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1353
                                                                                                                                 100.0%; Score 51;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alhopuro P, Ka.
Tuomainen T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human alpha2B-adrenoceptor (alpha2B-AR)
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                                                                                                          Mismatches
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T, Lakka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                DB 5;
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                                                                                                                                                             Length 1353;
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Nyyssoenen
                                                                                                          Indels
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AAD44389
ID AAD4
XX AAD4
AC AAD4
XX AAD4
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XX Huma
XX Huma
XX Hype
XX Homx
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ARESULT 4
AAQ14151
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XX Neux
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha -2B-adrenoceptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1353 BP; 223 A; 459 C; 405 G; 266 T; 0 U; 0 Other;
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     Homo sapiens
                                                    Neurotransmission;
                                                                                                                                                           06-JAN-1992
                                                                                                                                                                                                        AAQ14151;
                                                                                                                                                                                                                                                          AAQ14151 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting a risk of hypertension and targeting treatment in a subject determining the pattern of alleles encoding a variant alpha-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salonen
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hypertension; hypotensive; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                      GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGTGT 930
                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                         (first
                                                                                                      beta
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/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                          DNA;
                                                    adrenaline;
                                                                                                      adrenergic
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                                                                                                                                                      entry.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                          ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51;
Pred. No.
                                                                                                      receptor
                                                    epinephrine; NGC-alpha2beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                      gene
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AAT59499
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Best Local :
                                      Hartig PR,
                                                                                                              30-OCT-1989;
30-MAY-1991;
                                                                 (SYNA-) SYNAPTIC PHARM CORP
                                                                                                                                                                     22-OCT-1992;
                                                                                                                                                                                                                                                    US5595880-A.
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                       Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; signal transduction; neurotransmitter; ligand; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human alpha-2b adrenergic receptor genomic DNA clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT59499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone NGC-alpha2beta was isolated from a human spleen genomic library screening with a fragment of the human 5-HTIA receptor gene. The gene be used to express recombinant receptor protein which can be used to produce antibodies for inhibition of receptor function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 2; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated DNA encoding human adrenergic receptor - acids encoding alpha, 2-beta adrenergic receptor,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-1989;
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                             Weinshank RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
(first entry)
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                                                                                                       89US-00428856
91US-00707604
                                                                                                                                                                 9208-00965040
                                                                                                                                                                                                                                                                                   Location/Qualifiers
288. .1751
/*tag= a
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288. .1752
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Pred. No. 0.0
0; Mismatches
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thes 0;
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Best Local S
Matches 51
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                                                                                                                                                                                                                                                                                                                              30-JAN-1998;
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The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number
                                                                                                                                                                      Combination of polynucleotide probes, useful as array elements microarray for monitoring the expression of a number of target polynucleotides.
                                                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; probe; ss; array element; Parkinson's disease; signalling pathway population; cancer; adenocarcinoma immunopathy; AIDS; asthma; neuropathy; Alzheimer's di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human signalling pathway polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic receptor (AAW1804), a member of the rhodopsin-like signal transducer family. It was isolated from a human spleen genomic library in the lambda vector Charon 28 by screening with a 1.6 by fragment of the human 5-encoding the alpha-2B adrenoceptor gene. Plasmid pNGC-alpha-2B comprising DNA have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-B, are deposited as ATCC CRI 10275. Membranes of such cells can used in boind to, the alpha-2B adrenorgic receptor. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2064 BP; 319 A; 696 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 2A-E; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assay for alpha-2b adrenergic receptor ligands - using membranes of cells expressing recombinant receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-107576/10.
P-PSDB; AAW11804.
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                                                                                                                                SEQ ID NO 1181; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 100.0%; S
Similarity 100.0%; E
51; Conservative 0;
                                                                                                                                                                                                                                                                                                                             Seilhamer JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Pred. No. 0.00056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adenocarcinoma; leukaemia;
Alzheimer's disease; micro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probe
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hes 0;
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RESULT 7
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease; autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   discovery and development, toxicological and carcinogenicity studies, forenestes and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNAs, cDNAs and genomic fragments and in research and diagnostic applications. The array can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia, immunopathies e.g. AIDS and asthma, neuropathies e.g. Alrbands and seture. The sequence represents a polynucleotide probe of the invention. Note: The sequence represents a polynucleotide form part of the printed specification but was obtained in electronic forms a directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human alpha 2b-adrenoceptor nucleotide SEQ ID NO:41.
New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                 19-DEC-2000; 2000US-0257144P.
                                                                                                                                                                                                                                                                                                                                                                                                              19-DEC-2001; 2001WO-US050107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABZ42624 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2072 BP; 316 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200261087-A2
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                                                                                                                                   2003-046718/04.
DB; ABP81780.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; de
                                                                                                                                                                                                                                                                                       LIFESPAN BIOSCIENCES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                          Rough CL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .00056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes antigenic peptides (I) comprising: (a) CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or a vidity for a particular GPCR. (I) can be used as GPCR modulators and in Gqne therapy. The antigenic peptides for GPCRs are useful in detecting an antibodies. The peptides and antibodies are also useful for detecting an antibodies. The peptides and antibodies are also useful for detecting the gresence or absence of corresponding GPCRs. The antigenic peptides for CC regeneration-related diseases, immunological related diseases, cell cc regeneration-related diseases, growth-related diseases, cell cc atherosclerosis, bacterial, fungal, protozoan or viral infections, concer. cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host consisty, depression, schizophrenia, dementia, mental retardation, memory asthms. The protozoan of the protozoan or viral infections, concer. Confidential retardation, memory antibodies are propertional describes, prain, psoriasis, mental retardation, memory arthms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 51
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention
                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3274 BP;
                                                         P-PSDB;
                                                                                                          Drmanac RT, Liu C,
                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                    WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS68926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS68926 standard; cDNA; 291 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1; 523pp; English.
                                                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                (HYSE-) HYSEQ INC
                                                                         2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGTGT
                                                         ABG04739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                novel human diagnostic protein #4730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       587 A; 979 C; 967 G;
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Pred. No. 0.0
0; Mismatches
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   mutations
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RESULT 9
AAZ23896
ID AAZ2
XX AAZ2
AC AAZ2
XX LOBC
CKW Clag
KW Clag
KW Spor
XX W Spor
X
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                                           Nucleic acids encoding proteins which influence for treating and studying bone disorders.
               Example 3; Page 161-189; 391pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                          WPI; 1999-601320/51
                                                                                                                                                                 Rosenthal A,
                                                                                                                                                                                                                                              27-MAR-1998;
                                                                                                                                                                                                  (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                     26-MAR-1999;
                                                                                                                                                                                                                                                                                                                              07-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                    W09950284-A2
                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                           LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine LOBO homologue genomic DNA fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAZ23896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ23896 standard; DNA; 49999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide sequences. (I) is useful as hybridisation probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 4730; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                          99WO-EP002055.
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91.7%;
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0; Mismatches
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Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     뫈
                                                                                                                                             Wirth
                                                bone development, useful
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RESULT 10
AAZ23891
ID AAZ23
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Sequence 49999 BP; 13210 A; 11814 C; 10825 G; 14150 T; 0 U; 0 Other;
                                   This invention describes novel nucleic acids (I; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The mucleic acid molecules, proteins and antibodies can be used in animals, especially a transgenic mouse for grene therapy. The methods associated with bone development, e.g. spondyloepiphysal dysplasia and in the method of the invention
                                                                                                                                                                                                                                                                                               Example 3; Page 69-97; 391pp; German.
                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding proteins which influence bone development, useful for treating and studying bone disorders.
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-601320/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27+MAR-1998; 98DE-01013799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ROSE/) ROSENTHAL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9950284-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOBO; long bones; bone development; bone extension; skull; osteopathic; diagnostic; pharmaceutical; gene therapy; transgenic animal; disease; spondyloepiphysal dysplasia; achondroplasia; murine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine LOBO genomic DNA fragment 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel nucleic acids (1; designated LOBO (long bones)) encoding proteins influencing bone development in mammals. The proteins of the invention reduce and/or inactivate bone extension (i.e. development), with exception of the skull and have osteopathic activity. The mucleic acid molecules, proteins and antibodies can be used in diagnostic or pharmaceutical compounds e.g. for gene therapy. The methods animals, especially a transgenic mouse for the srudy of diseases associated with bone development, e.g. spondyloepiphysal dysplasia and in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ23891 standard; DNA; 49999 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49999 BP; 13135 A; 11787 C; 10868 G; 14209 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rump A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Невв Ј,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41.6; DB 2;
Pred. No. 0.12;
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Query Match

81.6%;

Score 41.6;

DB 2;

Length 49999,

Pred. No. 0.12;

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ADA66349/c
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                                                                                                 This invention relates to a novel recombinant carcinoma-associated (CA) CC nucleic acid comprising a fully defined genomic, mRNA or coding sequences CC of mouse Rorc gene or human RORC gene, mouse mCG1538 or human gene BAT1, CC mouse Iqgapl gene or human IQGAP1 gene, mouse EQF29 gene or human CC hCG27579 gene, mouse MCG99110 gene or human hCG27579 gene, mouse MCG99110 gene or human hCG27579 gene, as given in CC cancer cells, preferably lymphatic, breast, prostate or pithelial cells. CC A compound which modifies the expression of the CA genes or bind to CC carcinoma-associated proteins (CAP) may have cytostatic activity and the gequences of the invention may enable the use of gene therapy or a CC development of an anticancer vaccine. Therefore the invention may be CC useful for diagnosis and treatment of carcinomas, especially lymphoma CC carcinoma, breast cancer and prostate cancer. The CA genes may also be CC useful as DA vaccines and for generating animal models of carcinomas. CC requence is that of the mouse Pp3cc gene genomic DNA ccc contention.
 Best Loc
Matches
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Matches 44; Conservative
                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    carcinoma-associated gene; CA gene; Rorc gene; mCG15938 gene; BAT1 gene; Iqgap1 gene; IQGAP1 gene; Zpf29 gene; hCG27579 gene; Kcnj9 gene; KCNJ9 gene; Ppp3cc gene; PPP3CC gene; mCG910 gene; hCG27579 gene; cancer cell; lymphatic cell; brostate cell; prostate cell; prostate cell; carcinoma-associated protein; CAP; cytostatic; gene therapy; anticancer; vaccine; carcinoma; lymphoma carcinoma; lymphatic cancer; breast cancer; prostate cancer; DNA vaccine; animal model; mouse; murine; ds; Ppp3cc.
                                                                     Sequence 68230 BP; 18765 A; 14103 C; 14728 G; 20634 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 110-120; 229pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel recombinant carcinoma-associated nucleic acid, useful for evaluating the effect of a candidate carcinoma drug, and for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-569168/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2001; 2001US-00034650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse Ppp3cc gene genomic DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-NOV-2003
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                    Similarity
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                81.6%;
91.7%;
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                Score 41.6; DB Pred. No. 0.12;
 Mismatches
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                                 Length 68230;
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RESULT 12
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                                                                                                                                                    The invention relates to recombinant carcinoma associated (CA) nucleic CC acid sequences from mouse and human (ADA)1482-ADA03094), and to CC carcinobinant carcinoma associated proteins (CAP) encoded by them. The CC invention also encompasses expression vectors and host cells comprising a CC cA nucleic acid, a polypeptide (especially an antibody) that specifically cC binds to the protein, and a biochip comprising CA nucleic acid or CC fragments thereof. The sequences of the invention were identified using CC oncogenic retroviruses, which insert into the genome of the host organism CC at random. Many of these do not carry transduced host oncogenes or CC pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host CC pathogenic trans-acting viral genes, meaning that cancer incidence is a Cd irect consequence of the effects of proviral integration into host CC protooncogenes. The CA nucleic acid sequences can be used to diagnose CC carcinoma (sepecially breast cancer, prostate cancer, lymphoma or CC leukaemia) or a propensity to carcinoma by determination of the sequence CC acides, proteins and antibodies are also useful as CC therapeutic agents and in screening and evaluating drug candidates. The CC present sequence represents a specifically claimed murine CA nucleic acid sequence of the invention. Note: The complete sequence data for this CC patent did not form part of the printed specification, but was obtained cid electronic format directly from WIPO at
                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant nucleic acid encoding carcinoma associated useful for preparing compositions for treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse; murine; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening; gene; ds.
                                                                                                                                                    Sequence 68233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1583; 245pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-DEC-2002; 2002WO-US041414
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                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66085
 44;
                                                                                            Similarity
                                     GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGAG 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carcinoma associated gene, SEQ ID NO:1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry
                                                                                                                                                    BP;
                                                                                                                                                    18767 A; 14103 C; 14729 G;
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                                                                                            81.6%;
91.7%;
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                                                                                            Score 41.6;
Pred. No. 0.
                                                                           Mismatches
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J.12;
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                                                                                                                                                    20634 T; 0 U; 0 Other;
                                                                                                            Length 68233;
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04-DEC-2003 ADB72803;

(first

ADB72803 standard; DNA; 68233

ВP

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RESULT 14
AAL38337/c
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Cerebroprotective; neuroprotective; cytostatic; Nogo receptor homologue; NgR3; axonal growth; central nervous system; CNS; cerebral injury; spinal cord injury; stroke; demyelinating disease; multiple sclerosis; monophasic demyelination; encephalomyelitis; Marchiafava Biggamai disease; multifocal leukoencephalopathy; panencephalitis; Spongy degeneration; Alexander's disease; Canavan's disease; metachromatic leukodystrophy;
                                                                                                          Complementary
                                                                                                                                    15-AUG-2002
                                                                                                                                                              AAL38337;
                                                                                                                                                                                      AAL38337
                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a mouse gene of the invention.
                                                                                                                                                                                                                                                                                                                            Sequence 68233 BP; 18767 A; 14103 C; 14729 G; 20634 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-2001; 2001US-00798586.
23-OCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-0093722.
20-DEC-2001; 2001US-00034650.
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                                                                                                                                                                                                                                                  88099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse Ppp3cc gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant nucleic acid, useful for treating carcinomas, lymphomas,
cers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                                                 44;
                                                                                                                                                                            standard; DNA; 215980 BP
                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                 GAGGATGAAGCTGAAGAGGAGGAGGAAGAAGAGGAGGAGGAGGAAGAAGAG 48
                                                                                                                                                                                                                               ds; cytostatic; gene therapy; vaccine; carcinoma; lymphomas;
; neoplasm; adenocarcinoma; sarcoma; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 631; 2304pp; English.
                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                            Conservative
                                                                                       strand of a genomic sequence encoding a mouse NgR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Engelhard
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91.7%;
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Pred. No. 0.
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RESULT 15
ABQ76418/c
ID ABQ76418 standard;
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                                                                                                                                                                                                                                                                             CC The invention relates to a Nogo receptor homologue polypeptide, NgR2 or Squence, or a 420, 461 or 392 amino acid LRRCT sequence, a 284 amino acid NTLRRCT cc sequence, at a 20, 461 or 392 amino acid sequence, all given in the crossing inhibition of axonal growth of a central nervous system (CNS disease, disorder or injury, NgR3 or its antibody is useful for creating cerebral injury, spinal cord injury, stroke, cc useful for treating cerebral injury, spinal cord injury, stroke, cc demyelinating disease, e.g. multiple sclerosis, monophasic panencephalitis, Marchiafava-Bignani disease, Spongy degeneration, cc mammal against NgR3 is useful for inducing an immune response in a cc parification of interacting, regulatory protein in two-hybrid or three-hybrid cc sequences of the invention are useful for screening for gene certain disorders, for genetic mapping, and for RFLP associated conditable. The NgR3 binding antibody is useful for solating and purifying and therapeutic purposes. The sequences of the invention are useful for screening for RFLP associated conditables are useful for producing non-human transgenic cand therapeutic purposes. The sequences of the invention and/or quantitation of NgR3, and for diagnostic conditions are useful for producing non-human transgenic conditions are useful for retaining or preventing unregulated cellular represents the
                                                                                                                                                                                                                                       Best
                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                  Query Match
S. cerevisiae BAX-associated cDNA fragment
                                       21-NOV-2002
                                                                    ABQ76418;
                                                                                                                                                                                                                                                                Sequence 215980 BP; 56872 A; 50995 C;
                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 16; Page 219-275; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel Nogo receptor homolog polypeptide, NgR2 or NgR3, useful for treating central nervous system disorder, cerebral injury, spinal
                                                                                                                                                                  19661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           injury, stroke, and demyelinating diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krabbe's disease; immune; bait transgenic animal; unregulated murine; ds.
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44; Conservative
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91.7%;
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cellular growth; cancer; tumour; mouse;
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                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel nucleic acid representing a synthetic CC Bax gene. The Bax gene of the invention is useful for identifying Bax-CC resistant yeast or fungi, identifying, or obtaining and identifying CC Candida spp. sequences that are differentially expressed in a pathway CC eventually leading to programmed cell death or identifying inhibitors or clinhibitor sequences of Bax-induced cell death or identifying inhibitors or clinhibitor sequences of Bax-induced cell death or identifying inhibitors or clinhibitor sequences of Bax-induced cell death or identifying inhibitors or clinhibitor sequences of Bax-induced cell death or identifying inhibitors or clinhibitor sequences of Bax-induced cell death or identifying inhibitors or clinhibitor sequences or for the gene therapy. The composition of the sociated nucleic acids, polypeptides, pharmaceutical compositions, antisense molecules and antibodies are useful as medicaments or in corporating a medicament for treating, preventing and/or alleviating compositions, as cancer, or for preventing appoptosis in certain diseases. The compounds or proparting a medicament for modifying the endogenic flora of humans and cother mammals. The vaccine is useful for immunising against yeast or companiant infections. Apoptosis-related diseases include autoimmune disease, concerning and infections related with viral infections or neurodegenerations. This sequence represents a polynucleotide associated with the Bax gene described in the disclosure of the invention
                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 43
  Human nucleic acid associated
                                        07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                      Sequence 1721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-2000; 2000EP-00870318
04-JAN-2001; 2001EP-00870002
09-JAN-2001; 2001EP-00870003
                                                                                                                  AAD55832 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 36; Fig 1; 344pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bax; Bax-resistance; cytostatic; fungicide; immunosuppressive; virucide; vasotropic; vaccine; gene therapy; proliferative disorder; cancer; apoptosis; fungal; yeast; infection; autoimmune disease; ischaemia; neurodegeneration; cell death; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-2001; 2001WO-EP015398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JANC ) JANSSEN PHARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-667002/71.
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                     GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RH,
                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                      BP; 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eberhardt
                                                                                                                                                                                                                                                                                                          79.6%;
91.5%;
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                                                                                                                                                                                                                                                                                                                                                                      A; 400 C;
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                                                                                                                                                                                                                                                                                                            Score 40.6;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Luyten WHML,
protein (NAAP) -3 cDNA.
                                                                                                                                                                                                                                                                                                                                                                      341 G; 479 T; 0
                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                  BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reekmans
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و
                                                                                                                                                                                                                                                                                          4.
                                                                                                                                                                                                                                                                                                                                                                      U; 0 Other;
                                                                                                                                                                                                                                                                                                                              Length 1721;
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                 585
                                                                                                                                                                                                                                                                                          0;
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Best Loc
Matches
                                                                                   Query Match
Best Local
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12-JUL-2001; 2001US-0305104P.
13-JUL-2001; 2001US-0305325P.
13-JUL-2001; 2001US-0305390P.
19-JUL-2001; 2001US-0306694P.
20-JUL-2001; 2001US-0306170P.
                                                                                                                                                                                                                                          epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome) disorders, or infections. It is also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of NAAP. The NAAP or its fragments are useful in screening compounds for which acts as their agonist or antagonist. The microarray is useful in monitoring or measuring protein-protein interactions, drugts agent interactions, and gene expression profiles. NAAP DNA is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acid associated proteins (NAAP) and their corresponding nucleic acid sequences. The invention is usefu in diagnosing, treating and preventing diseases or conditions associate with the decreased expression or overexpression of NAAP, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human nucleic acid associated proteins (NAAP), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burford N,
Barroso I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yde H, Baughn MR,
Ramkumar J, Li JX,
Burford N, Elliott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer; atherosclerosis; neurological; epilepsy; Huntington's disease; developmental disorder; antiinflammatory; enuroprotective; thyromimetic; Cushing's syndrome; infection; gene therapy; cytostatic; anticonvulsant; cerebroprotective; hypothyroidism; cell proliferative disorder; allergy;
                                                                                                                                                                 Sequence 2663 BP; 875 A; 497 C; 715 G; 576 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; nucleic acid associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE GENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2003006618-A2
                                                                                                                                                                                                                   therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2003-221732/21.
DB; AAE37016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Page 232; 260pp; English
1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGA 47
                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
237. .2444
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Human NAAP protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nardson TW, Warren BA, Grif,
, Emerling BM, Lal PG, Lu
K, Becha SD, Duggan BM, Sa
tt VS, Ison CH, Ding L, Bc
B, Walia NK, Hafalia AJA,
                                                                                                                                                                                                                     present sequence is human NAAP
                                                                              79.6%;
91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC.
                                                                              Score 40.6;
Pred. No. 0
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                                                                                DB
.21;
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Lu DAM, Forsythe I
M, Sanjanwala MM, Le
L, Borowsky ML, Yao
AJA, Nguyen DB, Lu )
                                                      4.
                                                                                                                                                                                                                           CDNA
                                                                                                          Length 2663;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yao MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee EA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is useful
                                                      Gaps
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930

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RESULT 17
AADO4761
ID AADO4761
AXX AADO4
AXX AADO4
AXX AADO4
AXX AADO4
AXX Human
XXX Homo
XXX Homo
XXX Homo
XXX Homo
XXX ET CDS
FT CDS
FT CDS
FT CDS
FT Y
FT SALOT
AXX (JUVA
XXX PAN (JU
                                                                                                                                                                                                                                     The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) off 12 glutamates, in an acidic stretch of C1 ls amino acids (amino acids 294-311), located in the third intracellular three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR C2 gene is located on chromosome 2. Alpha2-AR mediate many off the C3 gene is located on chromosome 2. Alpha2-AR mediate many of the C4 gene is located on chromosome 2. Alpha2-AR mediate many of the C5 gene is located on chromosome 2. Alpha2-AR mediate many of the C6 ginephrine. An antagonist of alpha2B-adrenoceptor is useful for treating C6 disease involving vascular contraction of coronary arteries and a C6 clinically expressed as coronary heat disease (CHD), unstable chronic C6 corm or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
                                                                                               Query Match
Best Local S
Matches 42
                                                                                                                                                                                              Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Page 24-26; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Snapir A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JUVA-) JUVANTIA PHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catecholamine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200129082-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          norepinephrine; epinephrine; therapy; vascular contraction; variant; coronary artery; coronary heat disease; CHD; chronic angina pectoris; acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human alpha2B-adrenoceptor (alpha2B-AR) variant
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1 GAGGATGAAGCTGAAGAGGAGGAGGAAGAAGAGGAGGAGGAGGAAGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-300318/31.
                                                                                                 l Similarity
42; Conser
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                                                                                            Conservative
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                                                                                                                                                                                           219 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /"tag= a
/products "Human alpha2B-adrenoceptor (alpha2B-AR)
variant protein"
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                                                                                                            78.8%;
93.3%;
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Tuomainen T,
                                                                                                                                                                                           459
                                                                                 Score 40.2; DB Pred. No. 0.26; 0; Mismatches
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                                                                                                                                                                                400 G; 266 T; 0
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T, Lakka
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                                                                                                                                                                              U; 0 Other;
                                                                                                                         Length 1344;
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Nyyssoenen
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RESULT 19
ABX90802
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AAD44388
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  Murine gene
                       07-MAY-2003
                                                                 ABX90802
                                                                                                                                                                                              Sequence 1344 BP; 219 A; 459 C; 400 G;
                                                                                                                                                                                                                      The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha
                                                                                                                                                                                                                                                                                                                            Detecting a risk of hypertension and targeting treatment in a subject determining the pattern of alleles encoding a variant alpha-2-
                                                                                                                                                                                                                    -2B-adrenoceptor variant DNA
                                                                                                                                                                                                                                                                                                   Disclosure; Page 24-26; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                     Salonen
                                                                                                                                                                                                                                                                                                                                                                                                                                         20-FEB-2001; 2001FI-00000323.
                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; hypertension; alpha-2B-adrenoceptor; A hypertension; hypotensive; variant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-DEC-2002
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                                                                                                                      088
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DB; AAE26633.
                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-2B-adrenoceptor variant DNA.
                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              880
                                                             standard;
                                                                                                           GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAA 924
                                                                                                                        GAGGATGAAGCTGAAGAGGAGGAAGAAGGAGGAGGAGGAGGAAGAA 45
trapped sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA; 1344 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGTGTGAA 924
                                                                                                                                                          Conservative
                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002WO-FI000113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .1344
                                                               CDNA; 223
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                                                                                                                                                                 78.8%;
93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Human alpha-2B-adrenoceptor variant protein"
                                                                                                                                                         0,
                                                             В₽
                                                                                                                                                                 Score 40.2;
Pred. No. 0
                                                                                                                                                      Mismatches
                                                                                                                                                                                           266 T; 0 U; 0 Other;
                                                                                                                                                                 . 26;
                                                                                                                                                                           DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR; antihypertensive;
                                                                                                                                                                       Length 1344;
                                                                                                                                                    Indels
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                                                                                                                                                 Gaps
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(GTS)

SEQ Ħ

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RESULT 20
AAS75432
ID AAS75
XX AAS75
XX AAS75
XX 13-FE
XX UAAS75
XX Human
KW Hood
XX Human
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                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel murine cDNAs produced using gene trap technology. The OMNIBANK gene trapped sequences (GTSs) are individually identified novel genes, and are useful in functional genomic analysis, in the discovery and development of new therapeutic and disgnostic agents, for gene discovery, for disgnostic gene expression analysis, for cross species hybridisation analysis, and for genetic manipulations such as antisense inhibition or gene targeting. The polynucleotides of the invention are also useful for isolating cDNAs, genomic clones or full-length genes/polynucleotides, or their homologues, genomic clones or full-length genes/polynucleotides, or their homologues, theterologues, paralogues or orthologues, that are capable of hybridising to one or more of the new murine polynucleotide sequences. The polynucleotides are also useful for identifying the coding regions of the murine genome, and as hybridisation probes. ABX90657-ABX91862 represent the murine GTSs of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 43
                                                                      DNA encoding
                                                                                                            13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 223 BP; 64 A; 31 C; 65 G; 48 T; 0 U; 15 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New murine polynucleotides comprising gene trapped sequences, useful in functional genomic analysis, in the development of new therapeutic or diagnostic agents, for diagnostic gene expression analysis or for genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine; mouse; gene trap technology; gene trapped sequence; GTS; gene identification; functional genomic analysis; gene discovery; gene expression analysis; cross species hybridisation analysis; antisense inhibition; gene targeting; gene; ss.
             Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic of
                                                                                                                                                                                  AAS75432 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           electronic format directly from the USPTO web seqdata.uspto.gov/psipsDIDEntry.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 146; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-2000; 2000US-00728444.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Friedrich G, Zambrowicz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FRIE/) FRIEDRICH G.
(ZAMB/) ZAMBROWICZ B.
(SAND/) SANDS A T.
                                                                                                                                                                                                                                                                          14
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                                                                                                                                                                                                                                                                                                                                                  43
'
                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                             GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAGGAAGAG
                                                                    novel human diagnostic protein #11236.
                                                                                                          (first entry)
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                                                                                                                                                                                  CDNA;
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89.6%;
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Pred. No. 0.28;
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۲.
                                                                                                                                                                                                                                                                                                                                                                                     Length 223;
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                 disorder; ss
                                  forensic;
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RESULT 21
ABQ98152/c
ID ABQ981
XX
AC ABQ981
XX
DT 30-OCT
XX
MOUSE
XX
MOUSE;
XW MOUSE;
XW MOUSE;
XX
OS MUS SE
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                                                                                                                                                                                                                                                                                                                                                                                                                      CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, cand in recombinant production of (II). The polymucleotides are also used con diagnostics as expressed sequence tags for identifying expressed cc genes. (I) is useful in gene therapy techniques to restore normal cc extivity of (II) or to treat disease states involving (II). (II) is cc useful for generating antibodies against it, detecting or quantitating a cc polypeptide in tissue, as molecular weight markers and as a food cc supplement. (II) and its binding partners are useful in medical imaging cof sites expressing (II). (I) and (II) are useful for treating disorders cinvolving aberrant protein expression or biological activity. The cc involving aberrant protein expression or biological activity. The cc diagnostics, forensics, gene mapping, identification of mutations in cc diagnostics, for senetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and cc amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in celectronic format directly from MIDO at fine intention into intention into his or sequence.
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                 Mouse; ES cell;
development disc
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                 Mus sp
                                                                                                  Mouse ES cell related cDNA SEQ ID NO 1420.
                                                                                                                                  30-OCT-2002
                                                                                                                                                                                                    ABQ98152 standard; cDNA; 234 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 11236; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                  1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGAG
                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYSEQ INC.
                                                                                                                                                                                                                                                                                    ell; gene trapped
disorder; cell di
                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 117 A; 9 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is useful
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89.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ĭ
                                                 ed sequence; GTS;
differentiation
                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                    89 G;
                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      9 T;
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                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
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                                                   disorder; gene; s
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                                                                                                                                                                                                                                                                                                                                                                                   Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                      Other,
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US2002081668-A1

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RESULT 22
ABX90780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 43
                Murine; mouse; gene trap technology; gene trapped sequence; GTS, gene identification; functional genomic analysis; gene discovery;
                                                                                                                      Murine
                                                                                                                                                                   07-MAY-2003
                                                                                                                                                                                                                                              ABX90780 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 234 BP; 41 A; 64 C; 39 G; 87 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; SEQ ID NO 1420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel murine polynucleotides that individually identify novel genes which a retroviral gene trap vector has been integrated, useful in genomic analysis and in discovery, development of therapeutic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FRIE/) FRIEDRICH G.
(ZAMB/) ZAMBROWICZ B.
(SAND/) SANDS A T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1998;
01-DEC-1999;
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43; Conser
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                                                                                                                                                                                                                                                                                                                                trapped
                                                                                                                                                            (first
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                                                                                                                                                                                                                                            CDNA; 330
                                                                                                            sequence
                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0109302P.
99US-0168270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.4%;
89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29pp + Sequence Listing; English.
                                                                                             (GTS) SEQ ID No 124.
                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6,
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RESULT 23
ACD13226
ID ACD13
XX ACD13
AC ACD13
AC ACD13
XX IS CDNA

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Best Local (
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                                                                                                                                                                                                                                       ACD13226;
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                                                                                                                                                                                                                                                                                                                                                                                            113
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Claim 2; SEQ ID NO 124; 29pp;
                                  New murine polynucleotides comprising gene trapped sequences, useful in functional genomic analysis, in the development of new therapeutic or diagnostic agents, for diagnostic gene expression analysis or for genetic
                                                                                                                                                                                                                        (FRIE/) FRIEDRICH G.
(ZAMB/) ZAMBROWICZ B.
(SAND/) SANDS A T.
                                                                                                                                                                                                                                                                                                                                     30-NOV-2000; 2000US-00728444.
                                                                                                                                                                                                                                                                                                                                                                                                                             US2002161207-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression analysis; cross species hybridisation
antisense inhibition; gene targeting; gene; ss.
                                                                                                                                              2003-288124/28.
                                                                                                                                                                              Zambrowicz B,
                                                                                                                                                                          Sands AT;
English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analysis;
                                     for genetic
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CC trap technology. The OMNIBANK gene trapped sequences (GTSs) are
CC individually identified novel genes, and are useful in functional genomic
CC analysis, in the discovery and development of new therapeutic and
CC analysis, for cross species hybridisation analysis, for cross species hybridisation analysis, for cross species hybridisation analysis, and for gene expression
CC genomic clones or the invention are also useful for isolating cDNAs,
CC to one or more of the new murine polymucleotides or their homologues,
CC polymucleotides are also useful for isolating cDNAs,
CC to one or more of the new murine polymucleotides or their homologues,
CC polymucleotides are also useful for identifying the coding regions of the murine grows, and as hybridisation probes. ABX90657-ABX91862 represent
CC did not form part of the printed specification, but was obtained in
CC seqdata.uspto.gov/psinsDIDEntry hem)

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NOVX; autoimmune disease; allergy; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; multiple sclerosis; addiction; anxiety; pain; diabetes; glomerulonephritis; obesity; systemic lugus erythematosus; asthma; scleroderma; pancreatitis; graft versus host disease; ulcer; anaemia; cancer; trauma; infection; cardiomyopathy; atherosclerosis; hypertension; AIDS; Crohn's disease;
                                                                                                                         cDNA encoding novel human protein NOV37a.
                                                                                                                                                                                                                        ACD13226 standard; cDNA; 1173 BP
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 330 BP; 123 A; 59 C; 91 G; 54 T; 0 U; 3 Other;
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                              78.4%;
89.6%;
                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                              Score 40; I
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                           .28;
                                                                                                                                                                                                                                                                                                                                                          5,
                                                                                                                                                                                                                                                                                                                                                                                    Length 330,
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The invention describes an isolated NOVX polypeptide (I) comprising a CC 214, 395, 1098, 134, 427, 1333, 407, 806, 804, 1253, 382, 1045, 294, 496, CC 506, 759, 390, 133, 215, 240, 1069, 116, 439, 1138, 477, 316, 269, 219, CC 305, 406, 460, 365, 380, 829 or 326 amino acids fully defined in the CC specification, and the mature form of S1. (I) is useful for treating or preventing a pathology associated with (I) in a subject, preferably CC human, or for identifying an agent that binds to (I), where the agent is a cellular receptor or a downstream effector (I), a polynucleotide (II) CC encoding (I) or an anti-(I)-antibody (V) is useful treating or preventing CC disorders or syndromes such as autoimmune disease, allergies, Alzheimer's CC disease, stroke, Parkinson's disease, Huntington's disease, multiple CC disease, addiction, anxiety, pain, diabetes, glomerulonephritis, CC systemic lupus erythematosus, astima, scleroderma, graft versus host CC disease, pancreatitis, obesity, ulcers, anaemia, cancer, trauma, viral, CC disease, ill) or parasitic infections, cardiomyopathy, atherosclerosis, CC disease. (I), (II) or (V) is useful in screening assays, detection assays (e.g., chromosomal mapping, tissue typing, forensic biology), predictive CC medicine (e.g., diagnostic assays, and in methods of treatment (e.g., therapeutic and prophylactic). (II) is useful in gene therapy, to express CC (I), to detect NOVX mRNA or a genetic lesion in a NOVX gene, and to constant or or or only artivity. This segments encodes a novel burner NOV portein.
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07-JUN-2001; 2001US-029675P
11-JUN-2001; 2001US-0297414P
12-JUN-2001; 2001US-0297567P
18-JUN-2001; 2001US-0299530P
18-JUN-2001; 2001US-0299330P
19-JUN-2001; 2001US-0299330P
22-JUN-2001; 2001US-029930P
22-JUN-2001; 2001US-0300177P
26-JUN-2001; 2001US-0300187P
26-JUN-2001; 2001US-0301530P
28-JUN-2001; 2001US-0301550P
03-JUN-2001; 2001US-0301550P
03-JUN-2001; 2001US-0305801P
27-SEP-2001; 2001US-031580P
27-SEP-2001; 2001US-0315801P
27-SEP-2002; 2002US-031881P
27-SEP-2002; 2002US-031881P
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Padigaru M, I
Patturajan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as autoimmune disease, allergies, Alzheimer's disease, stroke, Parkinson's disease, Huntington's disease or multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acquired immunodeficiency syndrome; chromosomal mapping; tissue typing;
forensic biology; predictive medicine; gene therapy; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Baumgartner
Li L, Pena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002WO-US017558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kekuda R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203-204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spytek KA, Shen
r JC, Guo X, Gan
a CEA, Gorman L,
   This sequence encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shenoy SG, Mille
Gangolli EA, Ve
In L, Anderson DW,
   a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller CE, Hjar
EA, Vernet CAM;
son DW, Edinger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hjalt T;
protein
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Matches
                                                                                                                                                                                                                                                                                                                              04-JUN-2001; 2001US-0295601; 06-JUN-2001; 2001US-029561B; 06-JUN-2001; 2001US-029641B; 07-JUN-2001; 2001US-029675P; 17-JUN-2001; 2001US-029575P; 18-JUN-2001; 2001US-029952BP; 19-JUN-2001; 2001US-029952BP; 19-JUN-2001; 2001US-029930P; 21-JUN-2001; 2001US-029930P; 21-JUN-2001; 2001US-029930P; 21-JUN-2001; 2001US-0300177P; 22-JUN-2001; 2001US-0300183P; 28-JUN-2001; 2001US-030150P; 28-JUN-2001; 2001US-030150P; 28-JUN-2001; 2001US-030150P; 28-JUN-2001; 2001US-030150P; 28-JUN-2001; 2001US-030150P; 28-JUN-2001; 2001US-030150P; 27-SEP-2001; 2001US-0325685P; 27-SEP-2001; 2001US-0325685P; 22-JEB-2002; 2002US-0356814P; 2007US-0356814P; 20
                                                                                                                                                                   Zerhusen BD,
Gerlach VL,
Padigaru M,
Patturajan M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anxiety; pain; diabetes; glomerulonephritis; obesity; systemic lupus erythematosus; asthma; scleroderma; pancreatitis; systemic tursus host disease; ulcer; anaemia; cancer; trauma; infection; cardiomyopathy; atherosclerosis; hypertension; AIDS; Crohn's disease; acquired immunodeficiency syndrome; chromosomal mapping; tissue typing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOVX; autoimmune disease; allergy; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; multiple sclerosis; anxiety; pain; diabetes; glomerulonephritis; obesity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1173 BP; 326 A; 290 C; 339 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUN-2002;
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                                                                                                                                                                                                                                                                          (CURA-)
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                                                                                                        2003-140585/13.
DB; ABO07153.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                          CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                     Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                       Baumgartner
Li L, Pena
                                                                                                                                                                                                                                                                                                                   2002US-00161927
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                                                                                                                                                                                                                                     Kekuda
                                                                                                                                                                     Stone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA; 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
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                                                                                                                                                                                                                                ₽,
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89.6%;
                                                                                                                                                                                       Spytek KA,
JC, Guo X,
CEA, Gorman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein NOV37b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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Pred. No. 0.29
0; Mismatches
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                                                                                                                                                                                                           Shenoy SG, M
Gangolli EA,
                                                                                                                                                                                         ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                           Anderson DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
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                                                                                                                                                                                Miller CE, Hjalt A, Vernet CAM; on DW, Edinger SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
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                                                                                                                                                                                                                              Hjalt T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 addiction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Novel isolated NOVX polypeptide useful treating or preventing disorders or syndromes such as autoimmune disease, allergies, Alzheimer's disease, stroke, Parkinson's disease, Huntington's disease or multiple sclerosis

Claim

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RESULT 25
AAC38547
ID AAC38
XX AAC38
AC AAC38
AX Hybri
KW Hybri
KW Pronc
KW Pronc
KW Pronc
XX Arabi
XX Pronc
XX
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Best Local S
Matches 43
                                     25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
11-APR-1999;
21-APR-1999;
21-APR-1999;
23-APR-1999;
                                                                                                                                                                                                                                                                                                                               06-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                              25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana DNA fragment SEQ ID NO: 21366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC38547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1178 BP; 321 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA; 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGGATGAAGCTGAAGAGGAGGAGGAAGAAGAAGAAGAAG 48
                                                                                                                                                                                                                                                                                        2000EP-00301439
                                 99US-0121825P.
99US-0123548P.
99US-0123548P.
99US-0125788P.
99US-0126785P.
99US-0127462P.
99US-0127462P.
99US-0128234P.
99US-0129845P.
99US-0130077P.
99US-0130449P.
99US-0130449P.
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Pred. No. 0.29;
0; Mismatches
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ງ.29;
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             04-APR-1999
04-MAY-1999
05-MAY-1999
05-MAY-1999
06-MAY-1999
14-MAY-1999
14-MAY-1999
14-MAY-1999
14-MAY-1999
14-MAY-1999
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18-MAY-1999
16-MAY-1999
16-JUN-1999
16-JUN-1999
16-JUN-1999
18-JUN-1999
18-JUN
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28-APR-1999;
30-APR-1999;
99US-0130891P
99US-013248P
99US-01325P
99US-013421P
99US-013462P
99US-013945P
99US-014942P
99US-014082P
99US-014082P
99US-0141842P
99US-0141842P
99US-014433P
99US-014433P
99US-014433P
99US-014433P
99US-014433P
99US-014433P
99US-014433P
99US-014433P
99US-014433P
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RESULT 26
ABT20256
ID ABT2026
XX ABT20
XX ABPER
XX Pungi
KW Fungi
KW Cance
XX Asper

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Best Loc
Matches
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29-OCT 1999
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The invention relates to novel pessential genes of Aspergillus the invention are used to treat
                                                                                                                                              New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                                                                                                                                            Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                23-APR-2001; 2001US-0285697P.
27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-033899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aspergillus fumigatus
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                                                                                                                                                                                                                                                                                                                                                               (ELIT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match
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43; Conservative
                                                                                                                                                                                                                                                                                                                                                               ELITRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contamination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic;
                                                                                                Page;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fumigatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002WO-US013142
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89.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  essential gene; Aspergillus fumigatus; biofilm; antibody; immune response; ds
                                                                                                                                                                                                                                                                                                               Zamudio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2367
                                                                                                   English.
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Pred. No. 0.29
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,,</u>
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l purified or signatus. The fumigatus of the following the
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                                                                                                                                                                                                                                                                                                            Eroshkin
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or isolated nucleic acids of s. The isolated nucleic acids ent infections by a pathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 3
0.29;
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                                                                                                                                                                                                                                                                                                                  Lemieux
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99US-0145087P
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99US-0145218P
99US-0147303P
99US-015066P
99US-0151303P
99US-0153731P
99US-0159333P
99US-0159333P
99US-0159333P
99US-0159333P
99US-0159333P

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RESULT 27
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27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-0295890P.
09-UUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC subject (e.g. cancer), to prevent or contain non-infectious disease in a CC by A. fumigatus, or to prevent or contain contamination of an object (e.g. cancer), to prevent or inhibit formation on a surface of a CC by A. fumigatus, or to prevent or inhibit formation on a surface of a CC expressing recombinant protein for characterisation, screening or corganisms invade or reside, for comparing with the DNA sequence of A. CC sequences of identify duplicated genes or paralogues having the same or cc funigatus to identify duplicated genes or paralogues having the same or potential orthologous essential or virulence genes, for selecting and cc antigen to raise anti-ONA antibodies or to elicit another immune cc aitemates, for raising anti-protein artibodies, as an CC with which binding occurs or to identify interaction. The polypoptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively colorate correlative receptors or ligands in the case or virulence in which pathogenic organism invade or reside, and to cantered. This polymorphic sequence represents one of the sesential or correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or ligands in the case or virulence correlative receptors or li
                        Disclosure; Page; 175pp; English
                                        New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
                                                                                                                                                                                      Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                          (ELIT-)
                                                                                                                                                                                                                                                                                                                                                              23-APR-2002; 2002WO-US013142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
cancer; contamination; biofilm; antibody; immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200286090-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aspergillus fumigatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aspergillus fumigatus essential gene #3212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABT20854 standard; DNA; 2367 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism sucn ...
""hiect (e.g. cancer),
                                                                                                                                             2003-093124/08.
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                                                                                                                                                                                                                ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     μ
                                                                                                                                                                              Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2367 BP; 630 A; 644 C; 681 G; 412 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78.4%;
89.6%;
                                                                                                                                                                     Zamudio C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٥,
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 7;
Pred. No. 0.29;
                                                                                                                                                                 Eroshkin AM,
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                                                                                                                                                           Lemieux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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ABK65237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                  22-AUG-2000;
16+NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                     (MEND-)
                                                                                                                                                                                                                                                          22-AUG-2001; 2001WO-US026189
                                                                            (DUBE/)
                                                                                                (CREE/)
                                                                                                                                                                               18-APR-2001;
                                                                                                                                                                                                                                                                                                               28-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                     WO200215675-A1.
                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield;
                                                                                                                                                                                                                                                                                                                                                                                                                             fruit yield; growth rate; leaf senescence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis cDNA encoding a transcription factor #89.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABK65237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK65237 standard; cDNA; 2663 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2367 BP; 630 A; 644 C; 681 G; 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HEARD J.
JIANG C.
KEDDIE J.
                                                    MENDEL BIOTECHNOLOGY INC.
PILGRIM M.
CREELMAN R..
DUBELL A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGATGAAGCTGAAGAGGAGGAAGGAGGAGGAGGAGGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                   ; 2000US-0227439P.
; 2000US-00713994.
; 2001US-00837944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.4%;
89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB Pred. No. 0.29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7;
0.29;
                                                                                                                                                                                                                                                                                                                                                                                                               flower senescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T; 0 U; 0 Other;
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RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC encoding an Arabidopsis thaliana transcription factor, their variants, CC complements, fragments, or related polynucleotide with 31% to 95% CC sequence identity, where the plant polynucleotide with 31% to 95% CC sequence identity, where the plant, or the plant exhibits an altered CC phenotype as compared to a wild-type or reference plant, or the plant can be plant to the plant compared to a wild-type or reference plant, or the plant CC phenotype as compared to a wild plant. Also included CC are a transgenic plant trait as compared to a wild plant. Also included CC are a transgenic plant comprising the polynucleotides, a computer CC readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant Sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a computed control of the sequence or an antisense nucleic acid, inserting the CC encodes a polypeptide or an antisense nucleic acid, inserting the CC introducing the vector into a plant or a cell of a plant to overexpress control of the polypeptide or antisense nucleic acid, thereby production of control of a selecting for a modified trait (e.g. increased production of control of a plant to overexpress control of a plant by tolerance, herbicide resistence, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides encoding an A.
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                              Arabidopsis thaliana.
                                                                             plant; ss; gene; transcription factor;
plant breeding; pathogens resistance; pathogens
                                                                                                                               A. thaliana disease tolerance transcription factor cDNA, G1089
                                                                                                                                                                     23-SEP-2003
                                                                                                                                                                                                                                      ACD98382 standard; cDNA; 2663 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 1 of 232 isolated or recombinant polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 388-393; 941pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated or recombinant polynucleotide used \operatorname{plant}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pilgrim M, Creelman
Adam L, Ratcliff O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ADAM/)
(RATC/)
(REUB/)
(RIEC/)
(YUGG/)
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) RATCLIFF O.
) REUBER J L.
) RIECHMANN J L.
) YU G.
) PINEDA O.
                                                                                                                                                                                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                                                               3
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transcription factor
                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP;
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89.6%;
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uber JL, Riechmann JL,
                                                                               resistance; pests;
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             0.29;
                                                                                             disease resistance; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 658 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
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JL, Yu G,
                                                                                resistance
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7:
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Pineda O;
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                                                                                                                                                                                           The invention relates to a transgenic plant, comprising a recombinant polynucleotide that alters the plant's disease tolerance or resistance to when compared with the same trait of another plant lacking the crecombinant polynucleotide. The recombinant polynucleotide of any of so transcription factor proteins at least 6 consecutive amino acids of any of 56 transcription factor proteins consecutive amino acids of any of 56 transcription factor proteins consecutive amino acids of any of 56 transcription factor proteins consecutive amino acids of aplant (by: (a) transformed plants; and (c) the selecting a plant; attains a plant polynucleotide, (c) comparing the database sequence with the polypeptide or polynucleotide cited above; (c) selecting a database sequence that meets the selected sequence criteria; and (d) transforming the selected database sequence (c) approviding a test polynucleotide; (b) hybridising the test polynucleotide at low stringency with the recombinant polynucleotide in a plant to alter a trait of the plant. The transgenic plant is useful in plant breeding, particularly for generating plants with improved tolerance or resistance to mathogens and polants. The
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                                                                                                                          Sequence 2663 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 45-46; 124pp; English.
                                                                                                                                                                   for increasing tolerance or resistance to pathogens and pests. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-521768/49.
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                                                                                                                                      The invention relates to a number of isolated Arabidopsis thaliana cDNA sequences and their encoded proteins which are especially transcription factor related cDNA's and proteins. The isolated or recombinant plant producing transgenic plants with commercially valuable properties, i.e. modified or altered desirable traits as compared to a reference plant, such as an alteration in a plant growth characteristic, e.g. growth rate, flower senescence. Sequence information related to the polynucleotides and polypeptides can also be used in bioinformatic search methods. The transgenic plant is useful for growing a progeny plant from a parent plant. This sequence represents one of the cDNAs of the invention.
                                                                                                               Sequence 2663 BP; 836 A; 544 C; 625 G; 658 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 256; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                       New plant transcription factor polynucleotides and polypeptides, useful in producing transgenic plants with commercially valuable properties, such as an alteration in a plant growth characteristic, e.g. growth rate
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P-PSDB; ADD30228.
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Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O,
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19-NOV-2001; 2001US-0336045P.
11-DEC-2001; 2001US-0338692P.
14-JUN-2002; 2002US-00171468.
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seed germination rate; plant vigor; seedling vigor.
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ECAA2BAR  Horse alpha2 adrenergic receptor gene fragment probably subtype b, AL606560.  AL606560.1 GI:15591917 GSS, Alpha2 adrenergic receptor gene. Equus caballus (horse) Equus caballus (horse) Elikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammalia; Eutheria; Perissodactyla; Equidae; Equus. Alpha2 adrenergic receptor gene.  Hunter, C. and Elgar, G. Alpha2 adrenergic receptor gene 2 (bases 1 to 872) Hunter, C. Direct Submission	Match Local Similarity 100.0%; Score 51; DB 29; Length 1353; es 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  1 GAGGATGAAGATGAAGAGGAAGAAGAGGAGGAGGAGGAGG	/organi /mol_ty /db_xre <1:/	Õ	Clark, A.G., Glanows, Todd, M.A., Tanenbaur, Ferriera, S., Wang, G., Adams, M.D. and Carginates to the Company of the Company	Todd, M.A., Ferriera, S. Adams, M.D. Inferring r gene trios Science 302 14671302	-	AY416856 NV Homo sapien genomic sur AY416856	Page 2  ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                 library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clonef may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 63 row: A column: 7
Seq primer: SP6 Class: BAC ends.
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Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999) Other_GSSs: RPCI-23-63A7.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (Dases 1 to 430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.,
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Kr
Jong,P. and Fraser,C.M.
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GSS.
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AZ223727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (14-SEP-2001) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. UK Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 301 838 0200
Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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12 Medical Center Dr., Rockville, MD 20850,
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             /clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
RCORI; Site 2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10000"
/clone="RPCI-23-63A7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Equus caballus"
/mol_type="genomic DNA"
                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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The Institute for Genomic Research
9712, Medical Center Drive, Rockvill
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: hhlee@tigr.org
Seq primer: M13-21
                                                                                                                                                                                                                                            403
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UI-R-BO1-aqb-a-11-0-UI 3', mRNA sequence.
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                                                  Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                     1 GAGGATGAAGCTGAAGAGGAGGAAGAGGAGGAGGAGGAGGAAGAG 48
           1 (bases 1 to 517)
Bonaldo, M.F., Lenno
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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EST198860 Normalized rat brain,
 Normalization and
                                       Rattus.
                                                                                                                      BE097734.1
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                                                                                                                                                                                                                                                                                                                                                                /clone lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT7T3Pac; Site_1: |
Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus sp."
/mol_type="mRNA;"
/mol_type="mRNA;"
/db_xref="taxon:10118"
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91.7%;
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91.7%;
            Lennon, G. and Soares, M.B.
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Pred. No. 43;
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Pred. No. 43;
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sp. cDNA clone
                                                                Euteleostomi;
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SOURCE
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Sus scrofa (pig)
Sus scrofa
Sus scrofa
Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 552)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,
Nonneman, D.J., Wray, J.E. and Keele, J.W.
Porcine EST collection using a normalized library constructed from
embryos representing early developmental stages
                                                                                                                                                                                                                                 CF795982 MARC 4PIG Sus scrofa cDNA 3', mRNA linear CF795982 (F795982 GF795982.1 GI:37800555
                                                                                                                                                                                                                                               1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAAGAAGAG 48
                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Dento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first tall. The sequence tag present in the cDNA between the refore this may represent a bonafide poly a normalized corpus-striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through elements were found in this cDNA sequence: 365-436,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road , 4156 MEBRF, Iowa City, IA 5224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 319 335 8250
Fax: 319 335 9565
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97044477
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                                                                                                                                                                                                                                                                                                                                                                             TAG_TISSUE=corpus-striatum
TAG_LIB=UI-R-BO1
                                                                                                                                                                                                                                                                                                                                                            TAG_SEQ=CTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="sprague-Dawley"
/db xref="taxon:10116"
/clone="UI-R-B01-aqb-a-11-0-UI"
/dev stage="adult"
/lah-k-age="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/mol_type="mRNA"
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clone_lib="UI-R-B01"
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91.7%;
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Pred. No. 44;
0; Mismatches
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87 GAGGACGAAGAGGAAGAAGATGAGGAGGAGGAGGAGGAAGAG 40
                   l (bases 1 to 604)
Bullelle,F., Panchout,M., Lebon
Effect of xenobictics on the t.
Dreissena polymorpha
Unpublished (2002)
                                                                                           Similarity
                                                                                                                                                                                                                    Laboratory of Ecotoxicology
University of Le Havre
25 rue P. Lebon, 76058 Le Havre CEDEX, France.
Location/Qualifiers
                                                                                                                                                                                                                                                                                      Contact: Danger J-M
                                                                                                                                                                                                                                                                                                                                                           Dreissena polymorpha
Dreissena polymorpha
Bukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 GAGGATGAAGATGAAGAGGAGGACGAGGACGAGGAGGATGAAGAG 105
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AJ517718 Dreissena polymorpha
chron35, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ517718.1 GI:25778429
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                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
plate: TWW8018 row: D column. 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                             /organism="Dreissena polymorpha"

/mol_type="mRNA"

/db_xref="taxon:45954"

/clone="chron35"

/clone_lib="Dreissena polymorpha mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/ti8sue_type="pooled"
/lab_host="DHIOB"
                                                                                     81.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
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r: TAGAAGGCACAGTCGAGG.
Location/Qualifiers
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91.7%;
                                                               Score 41.6; DB
Pred. No. 45;
0; Mismatches
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Pred. No. 44;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604 bp
                                                                                                                                                                                                                                                                                                           Leboulenger,F. and Danger,J.-M.
                                                                                       _ DB 9;
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Dreissena polymorpha cDNA clone
                                                               4.
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                                                                                   Length 604;
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JOURNAL
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Best Local Similarity
Matches 44; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
Partition of the management of the mana dinear EST 15-JI pgfln.pk007.124 normalized chicken fat cDNA library Gallus gacdna clone pgfln.pk007.124 5 similar to gi|4506411 ref|NP 002874.1| Ran GTPase activating protein 1; Fugl (Homo sapiens) gi|11418178 ref|XP 010014.1| Ran GTPase activating protein 1; Fugl (Homo sapiens) sp|P46660|RGP1_HUMAN RAN GTPASE ACTIVATING professional profe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 102 row: K column: 10
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Contact: Shaying Zhao
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AZ288043.1 GI:9529829
GSS.
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Clones are derived from the mouse BAC library RPCI-23. For BAC
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Jong,P. and Fraser,C.M.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
|strain="C57BL/6J"
|db_xref="taxon:10090"
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/mol_type="genomic DNA"
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91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 4 row: L column: 16
                                                                                                                                                                     Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH309086 668 bp DNA linear GSS 03-DEC-20
CH230-4L16.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
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Cogburn, L.A., Morgan, R.W. and
Chicken ESTs from fat
                                                                                                                                                                                                                                                                                                          Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                                                                                                                                                                                                                                                                                                                                  Zhao,S., Shetty,J., Shatsman,S., Tse
Shvartsbeyn,A., Gebregeorgis,E., Ove
Riggs,F., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
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Townsend Hall, Newark, DE 19717, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Contact: Larry A. Cogburn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 302-831-1335
Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 668)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cogburn@udel.edu, www.chickest.udel.edu.
Location/Qualifiers
row: L
er: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab host="E.coli EMDH108"
/clone_lib="normalized chicken fat cDNA library"
/note="Vector: pspORT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9031"
/clone="pgf1n.pk007.124"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'tissue_type="fat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GI:14475309
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91.5%;
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                                                                                                                                                                                                                                                                                                                                                       Tsegaye,G.,
Overton,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BB
                                                                                                                                                                                                                     MD 20850,
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Russell, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226
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Class:

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Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.

Phasianinae; Gallus.

1 (bases 1 to 723)

Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Rong, W. T., Tickle, C., Brown, W. R. A., Wilson, S. A. and Hubbard, S. J. Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                              PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                            Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BU121352.1 GI:25331126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU121352
603146064F1 CSEQCHL17 Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGGATGAAGCTGAAGAGGAGGAAGAAGAAGAAGGAGGAGGAAGAAGA
                       /clone lib="CSBCHL17"
//note="Organ: kidney + adrenal; Vector: pBluescript II
KS(+); Site_1: EcoRI, Site_2: Not1; Modification of
BBluescript II KS(+) [Stratagene] vector to accommodate
uni-directionally cloned cDNA libraries from messenger RNA
IO.S. Patent # 6,387,624). Cut pBluescript II KS(+)
NotI and EcoRI. Ligate in double stranded adaptor
containing BsgI and BamHI sites
                                                                                                                                                                                                                                                                                                                                                                 Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                         /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                         /clone="ChEST145016"
/sex="Female"
                                                                                                                                                                                                                                                                  /strain="Compton Line 151"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                      /organism="Gallus gallus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-4L16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone 11b="CHOR1-230 Segment 1"
/note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
CHOR1-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Rattus norvegicus"
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91.5%;
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Pred. No. 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nRNA linear EST 25-NOV-2002
CDNA clone ChEST145016 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burt, D.W., Bosch, E., and Hubbard, S.J.
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AQ875889
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AUTHORS
TITLE
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BE613618
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Saccharomyces cerevisiae
Saccharomyces cerevisiae
                                          cerevisiae
AQ875889
AQ875889.1
GSS.
                                                            AQ875889
797 bp DNA linear G
VI30F6 mTn-3xHA/lacZ Insertion Library, strain Y2278
cerevisiae genomic 5', genomic survey sequence.
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                                                                                                                                                                                                  1 GAGGATGAAGCTGAAGAGGAGGAGGAAGGAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9714 row: 1 column: 02
High quality sequence stop: 711.
Location/Qualifiers
                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 753)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE613618
753 bp n
601504406F1 NIH_MGC_71 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 91.5
43; Conservative
                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3906193"
/tissue_type="leiomyosarcoma"
/lab_host="pH108 (phage-resistant)"
/clone_lib="NH108 (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. c"
                                                GI:6288133
                                                                                                                                                                                                                                                                           79.6%;
91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [5'ggccgcgtgcagccccggatccgaaaaaaag]
[5'aattcttttttcggatccggggctgcacgc] "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:9895215
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91.5%;
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Pred. No. 72;
0; Mismatches
        (baker's yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 40.6; DE; Pred. No. 72; O; Mismatches
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                                                                                                                                                                                                                                                                             Length 753;
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3 Saccharomyces
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REFERENCE

AUTHORS

TITLE
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VERSION KEYWORDS

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SOURCE

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RESULT 11 BU121352 LOCUS

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164

ORIGIN

Matches

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260
                                                                                                                                                                                                     Riggs, F.,
Rat BAC E
                                                                                                                                                                                                                                                                                                                                                                                                                                                BZ227940 826 bp DNA
CH230-400D22.TJ CHORI-230 Segment 2 Ra
CH230-400D22, genomic survey sequence.
BZ227940 BZ227940.1 GI:23886481
                                                                                 Unpublished (1999)
Contact: Shaying Zhao
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Kumar A Michael Snyder, Dept. of Mol. Cell. and Dev. B Yale University P.O. Box 208103, New Haven, CT 06520-8103, USA Tel: 203 432 9949 Fax: 203 432 6161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene
                                            Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                        Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Riggs, F., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                Rattue norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: anuj.kumar@yale.edu
te of mTn-3xHA/lacZ insertion.
Seg primer: GGCCTTCTTTCTTTGGAAGTAC
Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ross-Macdonald, P., Roemer, T., Coelho, P.S.R., Agarwal, S., Kumar, A., desEtages, S.A., Choung, K.-H., Sheehan, A., Symoniatis, D., Jansen, R., Umansky, L., Heidtman, M., Nelson, K., Iwasaki, H., Kanada, D., Lugo, R., Hager, K., Miller, P., Roeder, G.S. and Snyder, M. Hager, K., Miller, P., Roeder, G.S. and Snyder, M. Large-Scale Analysis of the Yeast Genome by Transposon Tagging and
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpubl
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                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                   Rattus.
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                                                                                                                                                                                                                                                                                           (bases 1 to 826)
                                                                                                                                                                                                     BAC End Sequences from Library CHORI-230 MboI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disruption
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="mTn-3xHA/lacZ Insertion Library, strain Y2278"
/note="Vector: pHSS6-8al; A yeast genomic DNA library
without 2 micron or mitochondrial DNA was prepared in
pHSS6-Sal; genomic DNA was size-fractionated (DNA of
roughly 2-3 kb in length) prior to cloning. This library
was subsequently mutagenized with a mTn-3xHA/lacZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/strain="Y2278 - S288C background, cir(0) rho(0)"
/db xref="taxon:4932"
/lab_host="E. coli"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40.6;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   containing lacz,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus genomic clone
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                                                                                          20850,
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Russell, D.,
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BQ231724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           availability, please contact Pieter de Jong (pdejong@mail.cho.o) Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 400 row: D column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 873)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://image.llnl.gov
Plate: LLAM13316 row: m column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BQ231724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop: 703.
Location/Qualifiers
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/tissue_type="melanotic melanoma"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally. Primer: Oligo of Note in the state of the skin in the ski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SBNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pieter de Jong"
                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/db_xref="taxon:9606"
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/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
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/mol type="qenomic DNA"
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                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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                                                                                                                                                                                                                                             clone="IMAGE:6055864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell_type="Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .826
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Pred. No. 73;
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AUTHORS
TITLE
JOURNAL
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Best Local Similarity
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BM807097
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Best Local
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                                                             BB852469 RIKEN full-length enriched, B16 F10Y cells Clone G370007K15 5', mRNA sequence.
BB852469 RIKEN full-length enriched, B16 F10Y cells BB852469 RIKEN full-length enriched, B16 F10Y cells BB852469.1 GI:17093923
                            Mus musculus
                                   Mus musculus (house mouse)
                                                                                                                                                                                                                1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103
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Plate: LLAM12266 row: 1 column: 23
                                                                                                                                                                                             found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1362)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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BM807097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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AGENCOURT 6552940 NIH MGC 85 Homo sapiens cDNA clone
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43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                            /tissue_type="lymphoma, cell line"
/lab_host="DHIOB (phage resistant)"
/clone_lib="NIH_MGC_85"
/clone_lib="NIH_MGC_85"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE:5552038"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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91.5%;
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Pred. No. 78;
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itch,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
genes Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
(11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
Computer-based methods for the mouse full-length cDNA
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
further details.

e mouse tissues.
                                                                                                                                                                                                                                                                                75
                                                                                             BX519271 Sugano mouse kidney mkia Mus musculus cDNA IMAGE:192035, mRNA sequence.
Mus musculus
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
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                   musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="G370007K15"
/cell_type="B16 F10Y cells"
/clone_lib="RIKEN full-length enriched, B16 F10Y cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism≈"Mus musculus"
/mol_type="mRNA"
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                                                                  GI:32295277
                 (house mouse)
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88.0%;
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Pred. No. 74;
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                                 Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                   AZ208950 Ilnear GSS 31-AUG
AZ208950 Ilnear GSS 31-AUG
SP_0138_A2_C06_T7A Strongylocentrotus purpuratus
urchin, sperm genomic BAC library Strongylocentrotus purpuratu
genomic clone Plate=138 Col=12 Row=E, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: sugF, Primer sequence: CTTCTGCTCTAAAAGCTGCG.

Location/Qualifiers
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RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Mouse UnigeneSet - RZPD2 (RZPDLIB No.981)
                                                                                                                                       AZ208950.1 GI:8422136 GSS.
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                Strongylocentrotidae; Strongylocentrotus.
                                                                                                          Strongylocentrotus purpuratus
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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/note="Organ: kidney; Vector: pME185-FL3; Site 1: DraIII
(CACCATGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG), XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
conservated by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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/lab_host="DH10B"
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/clone="IMAGp998J204714 ; IMAGE:1922035"
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/mol type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
                                                                                                                                                                                                                                               Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment Unpublished (1999)
Other_GSSs: CH230-504N18.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
                                                                                                                            9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                      Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH230-504N18.TJ CHORI-230 Segment 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop:
Location/Qualifiers
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Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T.,
                                                                                                                                                                                                                                Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BZ152227.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              additional resources
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wray, G.A., Ettensohn, C.A., Lehrach, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: acameron@caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 799)
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urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon;7668"
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Pred. No. 8
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Lehrach,H., Britten,R.J, Davidson,E.H.
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Overton,L., Russell,D., Chen,D.,
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BZ249816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                      Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
(http://www.chori.org/bacpac/rat230.htm). For BAC library
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
Plate: 447 row: L column: 4

row: L column: 4
                                                                                                                                                                                                                                                                                   Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
7912 Medical Center Dr., Rockville,
Fax: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riggs F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                     Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Riggs,F., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaila; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EAC49816
CH230-447L4.TJ CHORI-230 Segment 2 Ra
CH230-447L4, genomic survey sequence.
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Class: BAC ends.
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                             /organism="Rattus norvegicus"
/mol types"genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-447L4"
/cell_type="Brain"
    /cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
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/Clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10116"
/clone="CH230-504N18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
|mol_type="genomic DNA"
|strain="BN/SSNHsd/MCW"
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88.0%;
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Russell,D., Chen,D.,
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AUTHORS
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VERSION
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Query Match formatty
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Unpublished (1999)
Other GSSs: RPCI-24-401L13.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
712 Medical Center Dr., Rockville, MD 20850, USA
GAGGATGAAGCTGAAGAGGAGGAGGAAGAAGAGGAGGAGGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                                  Clones are derived from the mouse BAC library RPCI-24. For BAC library variability, please contact Pieter de Jong Resources (http://www.chori.org/bacpac/pac/pac/from BACPAC Plate: 401 row: L Column: 13
Seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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BH108383.1 GI:14940389
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RPCI-24-401L13.TJ RPCI-24 Mus musculus genomic clone

RPCI-24-401L13, genomic survey sequence.
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                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //cell type="Spleen/Brain"
//cell type="Spleen/Brain"
/clone lib="RPCI-24"
/note=Tvector: pTARBAC1; Site 1: BamH1; Site 2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male CS7BL/6J
                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
| clone="RPCI-24-401L13"
| sex="Male"
                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                                        78.4%;
89.6%;
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CHORI-230 Rat (BN/S8NH8d/MCW) BĀC library produced by
Pieter de Jong"
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88.0%;
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Pred. No. 78;
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Pred. No. 80;
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                                                                                   Length 152;
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UI-M.FWO-cbi-b-15-0-UI.rl NIH BM
IMAGE:6809872 5', mRNA sequence.
CA315228
CA315228.1 GI:24533352
EST.
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Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC (page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 257 row: L column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Other_GSSs: RPCI-24-257L19.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH072396
BH072396.1 GI:14891993
GSS.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH072396
RPCI-24-257L19.TV RPCI-24 Mus mu
                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPCI-24-257L19, genomic survey sequence
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                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Spleen/Brain"
/clone lib="RPCI-24"
/clone lib="RPCI-24"
/note="Vector: pTARBAC1; Site 1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site 1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-257L19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                       78.4%;
89.6%;
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                                                                                                                                                                                                                                                                                                                                                                       Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bp DNA line musculus genomic
                                                                                                                                                  BMAP_FW0 Mus musculus
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78;
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                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                          cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 18-JUL-2001
                                                                                                                                                                              EST 09-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                    Gaps
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REFERENCE
AUTHORS
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AUTHORS
TITLE
                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 25
CF897938/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL COMMENT
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                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                             ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
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Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 330)
Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGAG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                CF897938 330 bp
A0231H07-5 NIA Mouse Embryonic
                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                    CF897938.1 GI:38164987
                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
CF897938
                                                                                                                                                                                                                                                                                                                                                                                                              subtracted)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The following repetitive elements were found in this cDNA sequence: 37-156, >(GGA)n#Simple repeat (matched compliment) 82-200, >(GAA)n#Simple repeat (matched compliment) 201-254, >(GGA)n#Simple_repeat (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="whole brain"
/dev stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH BMAP_FWO"
/clone_lib="NIH BMAP]
/clone_lib="NIH BCOR_IIB="NIH BMAP]
/clone_lib="NIH BCOR_IIB="NIH BMAP]
/clone_lib="NIH BMAP_IIB="NIH BMAP_IIB="NIH BMAP]
/clone_lib="NIH BMAP_IIB="NIH BMAP_IIB="NIH BMAP_IIB="NIH BMAP]
/clone_lib="NIH BMAP_IIB="NIH B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       program coordinator."
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/mol_type="mRNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:6809872"
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                                                                                                                                                                                                                                                                                                                                                                                                          330 bp mRNA linear EST 04-NOV-2003
NIA Mouse Embryonic Germ Cell cDNA Library (Long,
Mus musculus cDNA clone NIA:A0231H07 IMAGE:30731418 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 256
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89.6%;
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Pred. No.
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                                                                                                                     Euteleostomi; 

; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST 04-NOV-2003
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cDNA libraries from

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DEFINITION
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LOCUS
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Best Local S
                                                                                                                                                                                                                                                                      Matches
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MEDLINE
PUBMED
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                                                                                                                                                                                                 325
                                                         AL135731
DKFZp434H0531_r1 434 (synonym: htes3) Homo
                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAGGAAGAAGAGGAGGAGGAAGAAGAG 48
                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                          Similarity 89.6
43; Conservative
                                                                                                                                                                     Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: A0231 row: H column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 11 (9), 1553-1558 (2001)
21429098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV-SPORT6 (Invitrogen); Site 2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA). Intramylational Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). Genome Res. 1: 153-158 (2001). [PMID: 11544199]. Genome Res. 1: 1553-158 (2001). [PMID: 11544199]). Ref. cells were obtained from Dr. Brigid L.M. Hogan and RNA was prepared by Dr. Mark G. Carter (NIH/NIA-IRP). Es cell-guilfied FBS, 0.1mM non-essential amino sodium pyruvate, 0.1 mM beta-mercaptoethanol, and 10^7 synthesized with an Oligo(dT) primer [Invitrogen: 2.5 up of total RNA, treated with T4 DNA polymerase, and to Lone-linker LJ-Sal4, purified by phenol/chloroform, and to Lone-linker LJ-Sal4, purified by phenol/chloroform, and cDNAs were amplified by long-range high fidelity PCR using then purified by phenol/chloroform and Centricon 100. Then, the Ex Taq polymerase (Takara) with a primer Sal4-S. The then purified by phenol/chloroform and Centricon 100. Then procedure by Dr. Kazuhiro Kondo at AISIN Cosmos. Then the CDNAs were cloned into SalI/NotI site of transformed with the ligation mixture by the standard The library was constructed by Yulan Plao and Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop: 330
                                                                                                                                                                                                                                                                          78.4%;
89.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="embryonic day 8"
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[Long, subtracted]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57Bl6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="NIA:A0231H07 IMAGE:30731418"
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xref="taxon:10090"
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                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                  Score 40; DB
Pred. No. 86;
0; Mismatches
                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                  5.
                                                                                                                                                                                                                                                                              Length 330;
                                                             linear
sapiens
                                                                                                                                                                                                                                            Indels
                                                     EST 04-SEP-2003
CDNA Clone
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                  ACCESSIÓN
VERSION
KEYWORDS
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CD564037/c
LOCUS
                                                                                                                                                   JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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AUTHORS
TITLE
JOURNAL
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgun.grc.nia.nih.gov
Plate: B0473 row: A column: 03
                                                                                                               Contact: Dawood B. Dudekula
                                                                                                                                                                                   (bases 1 to 358)

Piao, Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.

Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324
                                                                                                                                                                             Genome Res. 11
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                    358 bp

80473303-5 NIA Mouse E6.5 Whole E

musculus cDNA Clone NIA:B0473A03

CD564037

CD564037.1 GI:31607930

EST.
                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No s1 sequence available.
This clone (DKRZp434H0531) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de;
Munich/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blum,H., Bauersachs,S., Mewes,W., Weil,B. and Wiemann,S.
EST (Blum,H., Bauersachs,S., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 331)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL135731.1 GI:6603918
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AL135731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="maxn.9606"
/clone="DKPZp434H0531"
/tisuse_type="testis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adull"
/lab_host="0H10B"
/lab_host="0H10B"
/clone lib="434 (synonym: hte83)"
/note="Vector: pSportl; Site_1: NotI; Site_2:
                                                                                                                                                             (9), 1553-1558 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78.4%;
89.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                            mRNA linear
Embryo cDNA Library
3 IMAGE:30445634 5',
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                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence
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(Long) Mus
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                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 365)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikeido,I., Osato,N., Salto,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batelov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
                                                                                                                                                                                                                                                                                                                                                           BY054209 arken full-length enriched, clone 1730076P21 5', mRNA sequence.
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                         BY054209
BY054209.1 GI:26159657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: M13 Reverse High quality sequence s POLYA=No.
                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI; Site_2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 7 embryos at 6.5-days
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         At 6.5-days postcoitum"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="NIA Mouse E6.5 Whole Embryo cDNA Library (Long)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="E6.5 whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="NIA:B0473A03 IMAGE:30445634"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40;
Pred. No.
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87;
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d, TIB-55 BB88 Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
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                                                                                                                                                                                                                                                                                    /strāin="BALB/c"
/db xref="taxon:10090"
/clone="1730076P21"
/cell_line="TIB-55 BB88"
/clone_lib="RIKEN full-length enriched, TIB-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/mol_type="mRNA"
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                                                                                                                                                   Score 40;
Pred. No.
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                                                                                                                                                                                  Length 365;
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AUTHORS
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                                                                 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Myazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Computational Analysis of Full-Length Mouse cDNAs Compared with
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genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
10 (11), 1757-1771 (2000)
Commuter-based methods for the manufacturer Genome Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORS Okazaki Y. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Butt, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Chothia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A., Gariboldi, M., Gissi, C., Godzik, A., Bardt, D., Brusic, V., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Namata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petroysky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Schomeider, C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sultana, R., Schneider, C., Semple, C.A., Secou, M., Shimada, K., Verardo, R., Wanger, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Yang, L., Yuang, Sawa, M., Yang, I., Yang, Sawa, T., Pukuda, S., Hara, A., Hashizume, M., Magisawa, M., Yang, Y., Watanabe, Y., Yang, L., Yang, Sawa, T., Pukuda, S., Hara, A., Hashizume, M., Mayazaki, A., Sakai, K., Sasaki, D., Shibata, K., Rogers, J., Birney, E. and Hayashizaki, Y., Sasaki, D., Shibata, K., Ragers, J., Birney, E. and Hayashizaki, Y., Sasaki, D., Shibata, K., Ragers, J., Birney, E. and Hayashizaki, Y., Sasaki, D., Shibata, K., Ragers, J., Birney, E. and Hayashizaki, Y., Sasaki, D., Shibata, K., Ragers, J., Birney, E. and Hayashizaki, Y., Sasaki, D., Shibata, K., Ragers, J., Birney, E. and Hayashizaki, Y., Sasaki, D., Shibata, K., Ragers, J., Birney, E. and Hayashizaki, Y., Sasaki, D., Shibata, K., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cpush.
Computer-based methods for the mouse full-length cDNA ancyclopedia: real-time sequence clustering for construction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 420, 563-573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Mus musculus
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BY168255 RIKEN full-length enriched, bone marrow
musculus cDNA clone 1830070009 5', mRNA sequence
BY168255
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA linear ... d, bone marrow macrophage Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230-0045, Japan
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CA538239/c
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                                                                                                                                                                                                                                                            National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov Plate: CO264 row: C column: 01 Seg primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                     Contact: Dawood B. Dudekula
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
Other_ESTs: C0264C01-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piao,Y., Kargul,G.J., Dudekula,D.B., Qian,Y., Tanaka,T., Lim,M.K.,
Luo,A. and Ko,M.S.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA538239
CO264C01-5N NIA Mouse 7.5-dpc Whole Embryo cDNA Library (Long) Mus musculus cDNA clone NIA:CO264C01 IMAGE:30016728 5', mRNA sequence.
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CA538239.1 GI:25079717
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology/Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 373)
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                                                                                                                                                                                                                                               quality sequence stop: 373
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/db_xref="niaEST:C0264C01-5N"
/db_xref="taxon:10090"
/clone="NIA:C0264C01 IMAGE:30016728"
/tissue_type="whole embryo including extraembryonic tissues at 7.5-days postcoitum"
/dev_stage="7.5-days postcoitum"
                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                             Location/Qualifiers
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="1830070009"
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                                                                                          /clone_lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
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US-09-456-7110-30
US-09-456-952-12
US-09-411-212-7
US-09-561-138-7
US-09-561-138-7
US-09-561-138-9
US-09-561-138-9
US-09-561-138-9
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US-09-561-138-9
US-09-561-138-1
US-09-661-138-1
US-09-661-
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Sequence 1181, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE
TITLE OF INVENTION: PATHWAY GENE EXPRES;
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS: ADDRESSE: INCYTE PHARMACEUTICALS, INCREMENTAL PHAR
                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-09-016-434-1181
                   COMPUTER READABLE FORM:
                                                                                 STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA
                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-620-312D-619
US-09-621-976-17540
US-09-917-987-257
US-09-915-38A-12
US-09-915-38A-12
US-09-9146-249A-81
US-09-146-249A-81
US-08-56-419-9
US-09-146-249A-45
US-09-146-249A-45
US-09-146-249A-45
US-09-146-249A-45
US-09-146-249A-45
US-09-146-249A-45
US-09-266-188B-45
US-09-266-185B-40
US-09-266-815B-40
US-09-266-815B-40
US-09-266-815B-40
US-09-266-815B-40
US-09-266-815B-41
US-08-357-492-31
US-08-357-492-31
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US-08-357-492-31
US-08-357-492-31
US-08-357-492-31
US-08-357-492-31
US-08-357-953A-8
US-09-357-014-6
3 US-08-316-859A-3
4 US-09-38-31-31-3
4 US-09-38-31-31-3
4 US-09-38-31-31-3
5 US-09-58-472-33-1
5 US-09-357-014-6
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US-08-697-766A-1
US-09-022-983-1
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Sequence 1, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 17540, Appli
Sequence 17540, Appli
Sequence 17540, Appli
Sequence 181, Appli
Sequence 201, Appli
                                                                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Heard, Jacqueline
APPLICANT: Heard, Jose-Luis
APPLICANT: Ricchmann, Jose-Luis
APPLICANT: Keddie, James
APPLICANT: Samaha, Raymond
APPLICANT: Samaha, Raymond
APPLICANT: Samaha, Raymond
APPLICANT: Thang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Yi, Guo-Liang
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Jiang, Cai-Zhong
TITLE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
FILE REFERENCE: MBI-O10
CURRENT APPLICATION NUMBER: US/09/533,029
ERALIER APPLICATION NUMBER: 60/125,814
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 2663
; OTHER INFORMATION: G1089 US-09-533-029-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1181:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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LIBRARY: GENBANK
CLONE: 9178197
US-09-016-434-1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 47 Patent No.
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Best Local S
Matches 51
                                               LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
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COMPUTER: IBM PC compatible
OBERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 51; DB 4; 1 ilarity 100.0%; Pred. No. 2.8e-05; Conservative 0; Mismatches 0;
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1668
LENGTH: 636
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-1668
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FRANCSEQ for Windows Version 3.0
SEQ ID NO 1668
LENGTH: 636
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity 87.5
Matches 42; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
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                                                                                                                APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
AITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FTI.E REFERENCE: 210121.478C15
FTI.E REFERENCE: 210121.478C15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
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o. 6509448
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                                                                       FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                                                                                                                                                                                                                         Vedvick, Tom
Carter, Darrick
                                                                                                                                                                                                                         Mannion, Jane
                                                                                                                                                                                                                                                                                                           Bangur, Chaitanya S.
Lodes, Michael A.
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Lodes, Michael
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                                                                                                                                                                                                                                                                                                                                             Wang, Tongtong
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Bangur, Chaitanya
                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09736457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.3%;
87.5%;
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89.6%;
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Pred. No. 0.019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38.4; DB Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                 LENGTH: 636
; TYPE: DNA
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-671-325-1668
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                                                                                                                                                                                                         SOFTWARE: Fat
SEQ ID NO 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.3%;
Best Local Similarity 87.5%;
Matches 42; Conservative
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Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
NUMBER OF SEQ ID NOS: 1668
                                                                                                                                                                                                                                                                  APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
FULL REFERENCE: 210121.478C12
FULL REFERENCE: 200121.478C12
FULL REFERENCE: 200121.4
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APPLICANT: Bangur, Chaitar
APPLICANT: Lodes, Michael
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 636
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Wang, Chaitanya S
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Vedvick, Tom
Carter, Darrick
Retter, Marc
                                                                                                                                                                                                                                           FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fanger, Gary
Vedvick, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter, Darrick
Retter, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.3%;
87.5%;
   75.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38.4; DB 4;
Pred. No. 0.045;
0; Mismatches 6;
   Score 38.4; DB Pred. No. 0.045
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                               4.
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Matches

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Conservative

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Mismatches

6

Indels

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Gaps

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US-09-220-132-31
; Sequence 31, Applicati
; Sequence 10, 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, p
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APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Lewis, Marcia E.
APPLICANT: Schlegel, Nobert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASTSEQ for Windows Version 3.0
LENGTH: 650
                                                                                        SOFTWARE: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:

NAME/KEY: misc_feature

LOCATION: (1) - (650)

OTHER INFORMATION: n = A,T,C or G

US-09-328-111-333
                                                                                                                                PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
                                                                                                                                                                                APPLICANT: Shyjan, Andrew W.

TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT

TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE

FILE REFERENCE: 07334-074001

CURRENT APPLICATION NUMBER: US/09/220,132

CURRENT FILING DATE: 1998-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Overy Match 75.3%; Score 38.4; DB 3; Length 650; Best Local Similarity 87.5%; Pred. No. 0.045; Matches 42; Conservative 0; Mismatches 6; Indels
                                                                                               NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSEQ for Windows Version 4.0
                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6262333
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 333,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Burgess, Christopher C. APPLICANT: Bushnell, Steven E. APPLICANT: Carroll III, Eddie APPLICANT: Catino, Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Endege, Wilson O. APPLICANT: Steinmann, Kathleen E. APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -09-328-111-333
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                                                                           1194
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         RESULT 10
US-08-860-038-16/c
; Sequence 16, App.
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                                                                                                                                                                                                                     ; STRANDEDNESS: single; TOPOLOGY: linear; MOLECULE TYPE; other nucleic acid; DESCRIPTION: /desc = "Oligonucleotide"
                                                                                                                                                                                                                                                                                            TELEPHONE: (610) 454-3816
TELEPAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 15
SEQUENCE CHARACTERISTICS:
LENGTH: 58 base pairs
TYPE: nucleic acid
                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 9
US-08-860-038-15
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-220-132-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/
FILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR9
ATTORNEY/AGENT INFORMATION:
NAME: CASSIFIC STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6287762
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE DOCKET NUMBER: ST940:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE CORRESPONDENCES: 25

CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CROUZET, Joel
APPLICANT: SCHERMAN, Daniel
APPLICANT: WILS, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 500 Arcola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
16, Application US/08860038
                                                                                             635 GÁGGÁGGÁAGGTGÁGGÁAGÁTGÁAGÁGGÁTGÁGGÁGGÁGGÁGGÁAGÁ 681
                                                                       41;
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6287762
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Similarity 87.2%;
41; Conservative
                                                                                                                                                    72.2%;
ilarity 85.4%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        (610) 454-3816
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                                                                                                                                                    0;
                                                                                                                                                          Score 36.8; DB 3; Length 58; Pred. No. 0.099;
                                                                                                                                                                                                                                                                                                                                                                                                                         ST94090-US
                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37.4; DB 4; Length 1194; Pred. No. 0.085;
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LENGTH:

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Gaps

Patent No. 6287762

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RESULT 11
US-09-580-923-15
; Sequence 15, Ap
; Patent No. 6319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Savitzky Esq., Martin F.
REGLSTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST94090-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
TELEPHONE: (610) 454-3808
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                            APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH
TITLE OF INVENTION: IMMOBILIZED OLIGONUCLECTIDE
FILE REFERENCE: 03804.0138-01
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 08/860,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/15162
PILING DATE: 16-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR95/01468
PILING DATE: 08-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 111
MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLECTIDE NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SCHERMAN, Daniel APPLICANT: WILS, Pierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 500 ... CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                  1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAAGAAGAG 48
                                                                                                                                                                                                                                      5, Application US/09580923 6319672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                    Wils, Pierre
Cameron, Beatrice
                                                                                                                                                                              Scherman, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Rhone-Poulenc Rorer Inc.
500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               other nucleic acid
/desc = "Oligonucleotide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36.8; DB : Pred. No. 0.099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 58;
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                                                                                                                                                                         US-09-894-998A-34/c
                                                                                                                                                                                           RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                      US-09-580-923-16
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LENGTH: 58
TYPE: DNA
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SEQ ID NO 15
LENGTH: 58
                                                                                                                    Sequence 34, Application US/09894998A Patent No. 6537555
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, App. 800 No. 631967
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
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PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCTI
PRIOR FILING DATE: 1995-11-08
NUMBER OF SEQ ID NOS: 36
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH
TITLE OF INVENTION: IMMOBILIZED OLIGONUCLECTIDE
FILE REFERENCE: 03804.0138-01
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
                                                  APPLICANT:
                                                                                  APPLICANT: Hosken, Nancy Ann
APPLICANT: Craig H. Day
                                                                      APPLICANT:
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   TITLE OF INVENTION:
                                     APPLICANT:
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                                                                      Craig H. Day
Davin C. Dillon
                                     Sleath,
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                                                    McGowan, Patrick
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Paul R.
COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
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US-09-163-285-3
                                                     Query Match
Best Local S
Matches 41
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
                                                                                                                                   FEATURE :
                                                                                                                                           MOLECULE TYPE:
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Best Local S
                                                                                                                                                                                                                            NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MN
TELECOMMUNICATION INFORMATION.
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/0
FILING DATE: June 24, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/163,285
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CURRENT FILING DATE: US/09/894,998A
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 661
                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Khodadoust, Mehran
TITLE OF INVENTION: NOVEL MSP-5 PROTEIN AND NUCLEIC ACID MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: HSV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 02109
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3, 620401
620401
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                                                         72.2%;
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                                         Score 36.8; DI
Pred. No. 0.12,
0; Mismatches
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Pred. No. 0.12;
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                                                   DB 3;
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NAME/KEY:

LOCATION:
US-09-163-285-1
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US-09-702-705-316
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                                                                                                                               Sequence
                                                                                                                  Patent No.
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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US-09-163-285-1
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMER: 60/09:
FILING DATE: June 24, 199:
ATTORNEY/AGENT INFORMATION:
NAME: MARCHATTON:
                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
FEATURE:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid-
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
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CORRESPONDENCE ADDRESS:
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                                                                                                   INFORMATION:
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                                                                                                                                                                  316,
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        Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
                                                           WANTION:
Wang, Tongtong
Wang, Chaitanya S
Thael A.
Fan, Liqun
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28 State Street
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/ENTION: NOVEL MSP-
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85.4%;
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24, 1998
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CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 316
SEQ ID NO 316
LENGTH: 1633
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-316
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US-09-736-457-316
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US-09-702-705-788
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US-09-702-705-788
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SEQ ID NO 788
LENGTH: 1633
TYPE: DNA
                                                                                                                                           Patent No. 6509448
GENERAL INFORMATION:
                                                                                                                                                         Sequence 316, Application US/09736457 Patent No. 6509448
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Best Local (
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Best Local Similarity 85.4%;
Matches 41; Conservative
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APPLICANT:
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TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
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                                                                                                                                                                                                                                                                                                                     Local Similarity
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5. 6504010
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l Similarity 85.4%;
41; Conservative
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Wang, Tongtong
Wang, Tongtong
Chaitanya S
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Vedvick, Tom
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Bangur, Chaitanya S.
Lodes, Michael A.
                                                       Fanger, Gary
Vedvick, Tom
Carter, Darrick
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Retter, Marc
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                            Retter, Marc
Mannion, Jane
Fan, Liqun
Wang, Aijun
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APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
ITITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 788
LENGTH: 1633
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; SEQ ID NO 316
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-316
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US-09-736-457-788
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Best Local Similarity 85.-
41; Conservative
                                                                                                                                                              Sequence 316, Application US/09614124B Patent No. 6630574
                                                                                                                                                GENERAL INFORMATION:
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Best Local Similarity 85.4%;
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Patent No. 650944
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APPLICANT:
APPLICANT:
                                                                APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
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APPLICANT:
                                    APPLICANT:
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                       APPLICANT:
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                                                                                                                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAAGAAGAG
: Mannion, Jane INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
                                  Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
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Vedvick, Tom
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Lodes, Michael A.
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Retter, Marc
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CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 316
LENGTH: 1633

TITLE OF INVENTION: DIAGNOS FILE REFERENCE: 210121.478C9

DIAGNOSIS OF LUNG CANCER

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APPLICANT: Bangur, Chaltanya S.

APPLICANT: Lodes, Michael A.

APPLICANT: Lodes, Michael A.

APPLICANT: Vedvick, Tom

APPLICANT: Vedvick, Tom

APPLICANT: Marc

APPLICANT: Mannion, Jane

ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND

FILE REFERENCE: 210121, 478C9

CURRENT APPLICATION NUMBER: US/09/614,124B

CURRENT FILING DATE: 2001-07-11

NUMBER OF SEQ ID NOS: 1668

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 1638

LENGTH: 1638
                                                                                                                                                                                                         RESULT 22
US-09-671-325-316
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                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-124B-788
                                                                                                                                                                GENERAL INFORMATION:
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US-09-614-124B-788
                                                                                                                                                                                     Patent No.
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; ORGANISM: Homo sapiens
US-09-614-124B-316
                                                                                          APPLICANT:
ITLE OF INVENTION: "COMPOSITIONS AND METHODS FOR THE THERAPY AND ITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
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Best Local (
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Lodes, Michael
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ur, Chaitanya S.
                                                                                                                        Chaitanya
Michael A.
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85.4%;
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85.4%;
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Pred. No. 0.12;
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Pred. No. 0.12;
0; Mismatches 7;
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APPLICANT: LOGE, APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/589,184
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 788
LENGTH: 1633
TYPE: DNA
ORGANISM: Homo Sapiens
US-09-671-325-788
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SEQ ID NO 316
LENGTH: 1633
TYPE: DNA
ORGANISM: Homo sapiens
US-09-671-325-316
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US-09-671-325-788
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                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 72.2%;
Best Local Similarity 85.4%;
Matches 41; Conservative
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APPLICANT: Bangur, Chaitanya
APPLICANT: Lodes, Michael A.
                                                                                                                                                                                                                                                             Patent No.
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Best Local Similarity
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CURRENT FILING DATE: 2000-09-26
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Lodes, Michael
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, Tongtong
mir, Chaitanya g
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Pred. No. 0.12;
0; Mismatches 7; Indels 0
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; ORGANISM: Homo sapiens
US-09-589-184-788
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; ORGANISM: Homo sapiens
US-09-589-184-316
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SEQ ID NO 788
LENGTH: 1633
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SOFTWARE: FastSEQ for
SEQ ID NO 316
LENGTH: 1633
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Best Local Similarity 85.4
Matches 41; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                             Sequence 1085, Application US/09620312D
Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.479C8
CURRENT APPLICATION UNMBER: US/09/589,184
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 827
SOFTWAREN FRANCE: 2007-68-05
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Zhang, Jie
Zhang, Jie
Ren, Felyan
Chen, Rui-hong
Chen, Qing A.
Thrman, Tom
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Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunqing
Ma, Yunqing
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Vedvick, Tom
Carter, Darrick
Retter, Marc
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Lodes, Michael A.
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di, Vinod
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85.4%;
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85.4%;
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; TYPE: DNA
; ORCANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOGATION: (346) ... (4926)
US-09-418-710-28
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FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/52,317
PRIOR APPLICATION NUMBER: 09/52,317
PRIOR APPLICATION NUMBER: 09/88,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOPTWARE: pt FL genes Version 1.0
SEQ ID NO 1085
LENGTH: 2817
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US-09-418-710-30
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CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR TILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
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SEQ ID NO 28
LENGTH: 5561
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.4
Conservative
GENERAL INFORMATION:
APPLICANT: Jones, N
TITLE OF INVENTION:
                                                      Sequence 30, Appli
Patent No. 6596482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity 85.4%;
Matches 41; Conservative
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Patent No. 6596482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jones, Michael TITLE OF INVENTION: TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Drmanac,
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LOCATION: (109)..(2817)
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                  199 GAGGATGCACAGGGTGAGGAGGAAGAGGAGGAAGAGGAGGAAGAG
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                                                                                                                                                                                                                 4 GATGAAGCTGAAGAGGAGGAAGAGAGGAGGAAGAGTGT 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version 4.0
                                                                             Application US/09418710
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                       Michael
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TRANSCRIPTIONAL REGULATOR

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Sequence 12, Application US/09356952

Patent No. 6117663

GENERAL INFORMATION:

APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Boriack-Sjodin, Ann
APPLICANT: Margarit, S. M.
APPLICANT: Margarit, S. M.
APPLICANT: Margarit, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
FILE REFERENCE: 600-1-228N
CURRENT APPLICATION NUMBER: US/09/356,952
EARLIER APPLICATION NUMBER: 00/093,631

EARLIER APPLICATION NUMBER: 60/093,631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOPTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 6114
TYPE: DNA
ORGANISM: Mus musculus
US-09-495-714C-5
                                                                                                                                                                                                                                                                                                          RESULT 30
US-09-356-952-12
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LENGTH: 5573

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (346)...(4938)
US-09-418-710-30
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US-09-495-714C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

72.2%; Score 36.8; DB 4; Length 6114;

Best Local Similarity 85.4%; Pred. No. 0.14;

Matches 41; Conservative 0; Mismatches 7; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: University Technologies International Inc.
TITLE OF INVENTION: RETINAL CALCIUM CHANNEL (ALPHA) 1F-SUBUNIT GENE
FILE REFERENCE: 45499.4 (formerly 45074.6)
CURRENT APPLICATION NUMBER: US/09/495,714C
CURRENT FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 72.2%;
Best Local Similarity 85.4%;
Matches 41; Conservative
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CURRENT APPLICATION NUMBER: US/09/418,710
PRIOR APPLICATION UNMBER: DCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR APPLICATION NUMBER: JP 9/116570
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
PRIOR FILING DATE: 1997-04-18
                                                                                                                                                                                                                                                                                                                                                          1 GAGGATGAAGCTGAAGAGGAGGAGGAAGAGGAGGAGGAAGAGAG 48
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      Beq
Beq
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1: /ggn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

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6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

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18: /cgn2_6/ptodata/2/pubpna/US09E_PUB.seq:*
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length: 2000000000
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Match Length
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1 gaggatgaagctgaagagga.....aggaggaggaggaagagtgt
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     Minimum Match 0%
Maximum Match 100%
Listing first 150 s
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   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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      US-09-825-923-3
14 US-10-007-870-3
14 US-10-001-073-1
15 US-10-305-720-1181
15 US-10-25-567A-41
16 US-09-972-5466-16
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18 US-09-728-444-1146
18 US-09-728-444-1146
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19 US-09-728-444-1146
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Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1181, Ap
Sequence 31, Appl
Sequence 16, Appl
Sequence 1, Appl
Sequence 1, Appli
Sequence 146, Appl
Sequence 147, Apple
Sequence 124, Apple
Sequence 124, Apple
Sequence 10213, Apple
Sequence 81, Apple
Sequence 81, Apple
Sequence 83, Apple
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10 US-09-864-761
Sequence 47976, A
Sequence 19415, A
Sequence 6204, App
Sequence 177, Appl
Sequence 177, Appl
Sequence 177, Appl
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Sequence 204, Appl
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Sequence 18355, Appl
Sequence 11597, Ap
Sequence 111750, Sequence 111750, Sequence 111750, Sequence 111750, Sequence 1892, Ap
Sequence 111750, Appl
Sequence 211751, Ap
Sequence 211751,
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US-09-825-923-3
'Sequence 3, Application US/09825923
'Patent No. US20010016338A1
'GENERAL INFORMATION:
'APPLICANT: Snapir, Amir
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0 14 US-10-116-712-178
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8 19 US-09-864-761-286
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19 US-09-884-761-3182
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US-09-925-300-817
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                                                                                                                                                                             US-10-077-870-3

IS-quence 3, Application US/10077870

Publication No. US20030003470A1

GENERAL INFORMATION:

APPLICANT: Salonen, Jukka T

TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof

CURRENT APPLICATION NUMBER: US/10/077,870

PRIOR APPLICATION NUMBER: US/2007-05-21

PRIOR APPLICATION NUMBER: FI 20010323

NUMBER OF SEO ID NOS: 10

SOFTWARE: PatentIn Ver. 3.1

LENGTH: 133

TYPE: DNA

ORGANISM: Homo sapiens
                                                                                          FEATURE:
| PEATURE: CIS | NAME/KEY: CIS | NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Koulu, Marki
APPLICANT: Koulu, Marki
APPLICANT: Koulu, Marki
APPLICANT: Scheinin, Mika
APPLICANT: Salonen, Ullamari
APPLICANT: Salonen, Jukka
APPLICANT: Thomainen, Tomi-Pekka
APPLICANT: Salonen, Timo A
APPLICANT: Lakka, Timo A
APPLICANT: Vyss'nen, Kristiina
APPLICANT: Valkonen, Riitta
APPLICANT: Valkonen, Riitta
APPLICANT: Valkonen, Veli-Pekka
ITITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoc
ITITLE OF INVENTION: NOMBER: US/09/825,923
ITITLE OF INVENTION NUMBER: US/09/825,923
PRIOR APPLICATION NUMBER: US/09/825,923
PRIOR APPLICATION NUMBER: 09/422,985
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 3
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 1353
TYPE: DNA
ORGANISM: Homo sapiens
LENGTION: (1)...(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
US-09-825-923-3
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Best Local S
Matches 51
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Conservative 0; Mismatches 0; Indels
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Similarity

100.0%; ilarity 100.0%; Conservative 0;

Score 51; DB 14; I Pred. No. 9.7e-06; Nismatches 0;

Length 1353; Indels

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RESULT 5
US-10-225-567A-41
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; Publication No. US20030113798A1
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Publication No. US20030113725A1

GENERAL INFORMATION:

APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION UNMBER: US/10/001,073

CURRENT FILING DATE: 2001-11-01

NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1181
LENGTH: 2072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1181, Application US/10305720 Publication No. US20040010136A1 GENERAL INFORMATION:
                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: Roush, Christine L.
TITLE OP INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressic
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
CURRENT FILING DATE: 2002-11-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/016,434 PRIOR FILING DATE: 1998-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
OTHER INFORMATION: Genbank ID No. US20040010136A1 g178197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH: 1353
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Pred. No. 9.7e-06;
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    FOR G PROTEIN-COUPLED RECEPTORS
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                                                                                                                                                                                                                                                     Sequence 16, Application US/09972546 Publication No. US20030124704A1 GENERAL INFORMATION:
           SEQ ID NO 16
LENGTH: 215980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: F
SEQ ID NO 31
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LENGTH: 3274
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Best Local Similarity
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                                                                                                                                                                              APPLICANT: CATE, RICHARD L.
APPLICANT: SAH, DINAH W.Y.
TITLE OF INVENTION: NOGO RECEPTOR HOMOLOGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
                                                                                                                      FILE REFERENCE: A116US
CURRENT APPLICATION NUMBER: US/09/972,546
CURRENT FILING DATE: 2001-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/034,650 CURRENT FILING DATE: 2002-07-23 PRIOR APPLICATION NUMBER: US 09/474,377 PRIOR FILING DATE: 1999-12-29 PRIOR APPLICATION NUMBER: US 09/798,586 PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Engelhard, Eric
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000128
                                                                    PRIOR APPLICATION NUMBER: 60/238,361
PRIOR FILING DATE: 2000-10-06
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Morris, David APPLICANT: Engelhard, E.
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                                                 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                   APPLICANT: STRITTMATTER, STEPHEN M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
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ORGANISM: Homo sapiens
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DNA
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Pred. No. 0.0037;
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ORGANISM: Mus sp.

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LANGE/KEY: modified base
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LOCATION: (1202). (7222)
LOCATION: (2322). (7222)
LOCATION: (3728). (3822)
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LOCATION: (3823). (38222)
LOCATION: (3823). (38222)
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LOCATION: (3923). (38222)
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NAME/KEY: modified base
LOCATION: (51380)...(51479)
NAME/KEY: modified base
LOCATION: (56740)

VITHER INFORMATION: a, t, c, g, ot
LOCATION: (56740)

NAME/KEY: modified base
LOCATION: (56765)...(56864)
NAME/KEY: modified base
LOCATION: (66518)...(62917)
OTHER INFORMATION: a, t, c, g, ot
LOCATION: (66518)...(68530)
NAME/KEY: modified base
LOCATION: (68534)...(68633)
NAME/KEY: modified base
LOCATION: (68534)...(68633)
NAME/KEY: modified base
LOCATION: (74552)...(74651)
NAME/KEY: modified base
LOCATION: (94552)...(68633)
NAME/KEY: modified base
LOCATION: (94591)...(68633)
NAME/KEY: modified base
COCATION: (94591)...(68618)
NAME/KEY: modified base
COCATION: (94591)...(68618)
OTHER INFORMATION: a, t, c, g, ot
LOCATION: (93791)...
NAME/KEY: modified base
COCATION: (93791)...
OTHER INFORMATION: a, t, c, g, ot
LOCATION: (93791)...
OTHER INFORMATION: a, t, c, g, ot
LOCATION: (93791)...
OTHER INFORMATION: a, t, c, g, ot
LOCATION: (95670)...(96573)
NAME/KEY: modified base
COCHER INFORMATION: a, t, c, g, ot
LOCATION: (96570)...(96573)
NAME/KEY: modified base
COCHER INFORMATION: a, t, c, g, ot
LOCATION: (96570)...(9655)
OTHER INFORMATION: a, t, c, g, ot
LOCATION: (96570)...(9655)
NAME/KEY: modified base
COCHER INFORMATION: a, t, c, g, ot
LOCATION: (96565)
OTHER INFORMATION: a, t, c, g, ot
LOCATION: (96570)...(96570)
OTHER INFORMATION: a, t, c, g, ot
LOCATION: (96570)...
NAME/KEY: modified base
COCHER INFORMATION: a, t, c, g, ot
LOCATION: (96616)
OTHER INFORMATION: a, t, c, g, ot
LOCATION: (96616)
OTHER INFORMATION: a, t, c, g, ot
LOCATION: (96616)
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LOCATION: (96613)
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LOCATION: (96616)
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LOCATION: (96613)
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LOCATION: (96616)
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LOCATION: (96616)
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OTHER INFORMATION: a, t, c, g, NAME/KEY: modified base LOCATION: (127063)...(127162) OTHER INFORMATION: a, t, c, g,

other or unknown

other or unknown

NAME/KEY: modified\_base LOCATION: (114527)..(114626)

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Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
            APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
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OTHER INFORMATION: a, t, c, g, other or unknown NAME/KEY: modified_base
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OTHER INFORMATION: a, t,
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OTHER INFORMATION:
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LOCATION: (192158)
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LOCATION: (164710)..(164809)
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LOCATION: (153242)..(153341)
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                                                                                                                                                                                                                                   Heinonen, Paula
Alhopuro, Pia
Karvonen, Matti
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Salonen, Riitta
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Scheinin, Mika
Salonen, Jukka T
                                                                                                                                                               Tuomainen, Tomi-Pekka
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"nen, Kristina
NUMBER: 09/422,985
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91.7%;
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Pred. No. 0.0035;
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; NAME/KEY: CDS
; LOCATION: (1)...(1341)
; OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
US-10-077-870-1
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                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                  Sequence 146, Application US/09728444 Patent No. US20020161207A1
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                                                 APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Archur T.
APPLICANT: Sands, Archur T.
TITLE OF INVENTION: No. US20020161207A1el Murine Polynucleotide Sequences
TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: LEX-0100-USA
CURRENT APPLICATION NUMBER: US/09/728,444
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR FILING DATE: 1999-12-01
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TITLE OF INVENTION: Method for detecting a risk of hypertension and uses thereof
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 10 SOFTWARE: PatentIn Ver. :
SOFTWARE: Fa
EQ ID NO 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
                                     NUMBER OF SEQ ID NOS: 1206
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LOCATION: (1)..(1341)
COTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Similarity 93.3%;
42; Conservative
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                 FastSEQ for Windows Version 4.0
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93.3%;
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APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020161207Alel Murine Polynucleotide Sequences
FILE REFERENCE: LEX-0100-USA
CURRENT APPLICATION NUMBER: US/09/728,444
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US/09/728,444
PRIOR APPLICATION UMMBER: US/09/728,444
SPRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 1206
SEQ ID NO 124
LENGTH: 330
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US-09-728-444-124
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Patent No. US20020081668A1
GENERAL INFORMATION:
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020081668A1el Mur
FILLE REFERENCE: LEX-0101-USA
CURRENT APPLICATION NUMBER: US/09/728,446
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,270
NUMBER OF SEQ ID NOS: 1461
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 234
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature;
LOCATION: (1)...(234);
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                   Sequence 124, Application US/09728444 Patent No. US20020161207A1 GENERAL INFORMATION:
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Best Local
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; LOCATION: (1)...(223)
; OTHER INFORMATION: n = A,T,C or G
US-09-728-444-146
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Best Local Similarity 89.6%;
Matches 43; Conservative
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    174 GÁGGÁGGÁÁGAGGÁÁGÁGGÁÁGÁAGÁGGÁAGÁGGÁAGÁGGÁÁGAÁGÁG
    127

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Pred. No. 0.013;
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Pred. No. 0.013;
0; Mismatches
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Mutant Animals Defined Thereby
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
VNUMBER OF SEQ ID NOS: 73128
JENGTH: 642
TYPE: DNA
OPGANTSM: Glucina may
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US-10-161-927-81
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                                                                                                                                                                                                                     GENERAL INFORMATION:
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US-10-425-114-10213
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Best Local :
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                                                                                                                                                                                    APPLICANT: Zerhusen, Bryan D.
APPLICANT: Kekuda, Ramesh
                                                                          PPLICANT
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                                                                                                                             PPLICANT
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Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: 700899387_FLI
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Best Local
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ORGANISM: Mus musculus
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LOCATION: (1)...(330)
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                                                                                                                                                                                                                                                                                                231 GÁGGÁTGÁGGATGAGGÁTGAGGÁTGÁGGÁGGÁGGÁGGÁGGÁÁGÁÁGÁG 278
                                                                                                                                                                                                                                                                                                                     43;
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Gangolli, Esha
Vernet, Corine
                                                                                                   Miller, Charles E.
Hjalt, Tord
Gerlach, Valerie L.
Baumgartner, Jason C.
                                                                                                                                                                                                                                                                                                                                                                                Similarity
Anderson,
          Gorman, Linda
                      Pena, Carol E.A.
                                                Padigaru, Muralidhara
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                                                                                                                                                                                                                           Application US/10161927
To. US20030235821A1
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Similarity 89.6%;
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                                                                                                                                           , Kimberly A. , Suresh G. , Charles E.
                                                                          Esha A.
                                                                                                                                                                                                                                                                                                                                                                   78.4%; Score 40; DB 12; Length 642; 89.6%; Pred. No. 0.012;
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Pred. No. 0.013;
0; Mismatches
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Patturajan, Meera

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)..(1166)
US-10-161-927-81
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SEQ ID NO 81
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Best Local Similarity
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                                                                   APPLICANT:
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TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 21402-377 D (Cura 677 Other)
CURRENT APPLICATION NUMBER: US/10/161,927
CURRENT FILING DATE: 2002-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 190
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PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/296,404
                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zerhusen,
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                                                   APPLICANT:
                                                                                                      APPLICANT
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                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
CANT: Anderson, David W.
CANT: Edinger, Shlomit R.
CANT: Patturajan, Meera
CANT: Stone, David J.
OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING
OF INVENTION: THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/298,528
FILING DATE: 2001-06-15
APPLICATION NUMBER: 60/325,685
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FILING DATE: 2001-06-11
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APPLICATION NUMBER: 60/299,133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/296,418 FILING DATE: 2001-06-06 APPLICATION NUMBER: 60/296,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-06-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAG
                                                                                                                                                                                                                                                                 Spytek, Kimberly A. Shenoy, Suresh G. Miller, Charles E.
                                                                                                                                             Padigaru, Muralidhara
                                                                                                                                                                Gangolli, Esha
Vernet, Corine
                                                                                                                                                                                                                 Baumgartner, Jason C.
                                                                                                                                                                                                                                    Gerlach, Valerie L.
                                                                                                Gorman, Linda
                                                                                                                                                                                                                                                                                                                  Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                  Carol E.A.
                                                                                                                                                                                                                                                                                                                                     Bryan D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78.4%;
89.6%;
                                                                                                                                                                                  Esha A.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                   THEM
                   AND METHODS
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; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_143329C.1
US-10-424-599-47976
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US-10-424-599-47976
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; LOCATION: (1)..(1141)
US-10-161-927-83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47976, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 47976
                                                                                                  Query Match
Best Local
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LENGTH: 1178
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Best Local
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223) B
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CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: 60/295,661
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/295,607
PRIOR APPLICATION NUMBER: 60/295,607
                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,575
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PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 60/296,418
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PRIOR FILING DATE: 2001-09-27
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PRIOR FILING DATE: 2001-06-15
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PRIOR APPLICATION NUMBER: 60/297,567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                             LENGTH: 1290
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                                                                                  43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                        1 GAGGATGAAGCTGAAGAGGAGGAAGAAGAGGAGGAGGAGGAAGAGAG 48
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Similarity 89.6%;
43; Conservative
                                                                                                    Similarity
                                                                                  Conservative
                                                                                                    78.4%;
89.6%;
                                                                                                      Score 40; DB 12; Length 1290; Pred. No. 0.012;
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Pred. No.
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                                                                                  Gaps
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GENERAL INFORMATION, BO
APPLICANT: Jiang, Bo
APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
CURRENT ENCENTION NUMBER: US/10/128,714
FILE REFERENCE: 10182-018-999
CURRENT EPLICATION NUMBER: US/10/128,714
FRIOR APPLICATION NUMBER: US 60/285,697
RRIOR APPLICATION NUMBER: US 60/285,697
RRIOR APPLICATION NUMBER: US 60/287,066
FRIOR APPLICATION NUMBER: US 60/303,899
FRIOR FILING DATE: 2001-00-08-31
                                                                                                                                   , ORGANISM: Aspergillus fumigatus
US-10-128-714-6204
                                  Best Local Similarity 89.6
Matches 43; Conservative
                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 8603
SOFTWARE: Patentin version 3.1
SEQ ID NO 6204
LENGTH: 2367
                                                                                                 Query Match
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; OTHER INFORMATION: Clone ID: LIB3150-014-B11_FLI
US-10-425-114-19415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6204, Application US/10128714 Publication No. US20030119013A1
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SEQ ID NO 19415
LENGTH: 1433
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Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: KOVALIC, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
NUMBER OF TITLE DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                    78.4%;
89.6%;
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89.6%;
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                     0; Mismatches
                             Score 40; DB 14; Length 2367; Pred. No. 0.012;
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Pred. No. 0.012;
0; Mismatches 5; Indels
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          Indels
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Gaps
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APPLICANT: Snamha, Raymond
APPLICANT: Zhang, James
APPLICANT: Yu, Guo-Liang
APPLICANT: Archiffe, Oliver
APPLICANT: Pilgrim, Marsha
APPLICANT: Pilgrim, Marsha
APPLICANT: Jiang, Cai-Zhong
TILTE OF INVENTION: DISEASE-INDUCED POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/533,029
EARLIER APPLICATION NUMBER: 60/125,814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jiang, Bo
APPLICANT: Tishkoff, Daniel
APPLICANT: Lemidux, Sebastien
APPLICANT: Lemidux, Sebastien
APPLICANT: Lemidux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
CURRENT FILING DATE: 1082-018-99
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Heard, Jacqueline
APPLICANT: Broun, Pierre
APPLICANT: Riechmann, Jose-Lui
APPLICANT: Keddie, James
APPLICANT: Pineda, Omaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-7204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3-09-533-029-47
Sequence 47, Application US/09533029
Publication No. US20030046723A1
GENERAL INFORMATION:
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Best Local s
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SEQ ID NO 7204
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US-10-128-714-7204
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Similarity 78.4%; Score 40; D
Similarity 89.6%; Pred. No. 0.
43; Conservative 0; Mismatche
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RESULT 22
US-10-225-068-65
J Sequence 65, Application US/10225068
Publication No. US20030217383A1
J GENERAL INFORMATION:
J APPLICANT: Mendel Biotechnology, In-
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                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
LOCATION: (31)..(2427)
; OTHER INFORMATION: G1089
US-09-934-455-177
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US-09-934-455-177
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 47
LENGTH: 2663
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                          Query Match
Best Local
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SEQ ID NO 177
                                                                                                                                                                                            Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/227439
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: MBI-0023
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pineda, Omaira
TITLE OF INVENTION: Genes for Modifying Plant
FILE REFERENCE: MBI-0025
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                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 2663
                                                                                                                           43,
                                                                                                                                             1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAAGAG 48
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                                                                                                                                                                                            43; Conservative
                                                                                                                                                                                                           Similarity
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Heard, Jacqueline
Jiang, Cai-Zhong
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o. US20030121070A1
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Biotechnology, Inc.
                                                                                                                                                                                                          78.4%;
89.6%;
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                                                                                                                                                                                                          Score 40; DB 10;
Pred. No. 0.012;
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US-10-302-267-45
APPLICANT: PILGTIM, MATSHA
APPLICANT: PILGTIM, ROBERT
APPLICANT: Creelman, Robert
TITLE OF INVENTION: PLANT GENE SEQUENCES II
FILE REFERENCE: MBI-0007
CURRENT APPLICATION NUMBER: US/10/302,267
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US/09/506,720
PRIOR PILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/120,880
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR APPLICATION NUMBER: 60/121,037
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-22
PRIOR FILING DATE: 1999-02-22
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CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR PILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
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SEQ ID NO 65
LENGTH: 2663
TYPE: DNA
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APPLICANT:
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Jiang, Cai-Zhong
Samaha, Raymond
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Reuber, Lynne
Zhang, James
                                                                                                                                                                                                                                                                                                                                                                                                                 fromm, Michael
Heard, Jacqueline
Heard, Jacqueline
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Adam, Luc
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Adam, Luc J.
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Heard, Jacqueline E.
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APPLICANT: YH, GUO-LIANG
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-06-09
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
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SEQ ID NO 45

LENGTH: 2663

TYPE: DNA

ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (31)..(2424)
US-10-302-267-45

US-10-302-267-45
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US-10-374-780A-229
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Publication No. US2004001927A1
GENERAL INFORMATION:
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/129,450
PRIOR APPLICATION PRIOR PRIOR
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Best Local Similarity
                                                                           OR APPLICATION NUMBER: 60/338,692
OR FILING DATE: 2001-12-11
OR APPLICATION NUMBER: 10/171,468
OR FILING DATE: 2002-06-14
OR APPLICATION NUMBER: 10/225,066
OR FILING DATE: 2002-08-09
APPLICATION NUMBER: 10/225,067 FILING DATE: 2002-08-09
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Broun, Pierre E
Pilgrim, Marsha L
Dubell III, Arnold
Pineda, Omaira
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Heard, Jacqueline E
Haake, Volker
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** APPLICANT: Jiang, Bo
APPLICANT: HJ, Wenqi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamdido, Carlos
APPLICANT: Lemieux, Sebassien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
CURRENT FILLRESTION: Methods of Use
CURRENT PAPLICATION NUMBER: US/10/128,714
PRIOR APPLICATION NUMBER: US/20/285,697
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR PILING DATE: 2001-07-99
PRIOR PILING DATE: 2001-08-05
PRIOR PILING DA
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US-10-128-714-5204
                                                                                                                                      Sequence 5204, Application US/10128714 Publication No. US20030119013A1 GENERAL INFORMATION:
APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
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US-10-128-714-204
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; OTHER INFORMATION: G1089
US-10-374-780A-229
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Best Local
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NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO 229
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TYPE: DNA
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D: US20030119013A1
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89.68;
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Pred. No. 0.011;
0; Mismatches 5; Indels
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FOR

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RESULT 28
US-09-864-761-18355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 17979
LENGTH: 191
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Best Local Similarity
Matches 43; Conserv
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APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
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PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR FILING DATE: 2001-06-05
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CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
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                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO CHR22 81.0
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.49
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.86
OTHER INFORMATION: NT HIT: 916168503, EVALUE 2.00e-31
OTHER INFORMATION: EST HUMAN HIT: BE392547.1, EVALUE 2.00e-07
OTHER INFORMATION: SWISSPROT HIT: P46060, EVALUE 2.00e-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
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FILING DATE: 2001-07-09
APPLICATION NUMBER: US 60/316,362
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                                                                                                                             1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAAGA 47
                                                                                                                                                                                         Similarity
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89.6%;
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Pred. No.
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Pred. No.
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US-09-864-761-18355
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SEQ ID NO 18355
LENCTH: 423
TYPE: DNA
  Matches
                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
                                                                                                                          OTHER INFORMATION: MAP TO ACO10133.1

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN HBL1A, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
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CURRENT FILING DATE: 2001-05-23
PRICE APPLICATION NUMBER: US 60/180,312
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: US 60/207,456
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                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                              Local Similarity
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-09-21
  42;
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Hanzel, David K.
Chen, Wensheng
  Conservative
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                         76.5%;
89.4%;
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                           Score 39; DB 9;
Pred. No. 0.024;
  Mismatches
                                                    Length 423
  Indels
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OTHER INFORMATION: MAP TO ACO10133.1

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.2

OTHER INFORMATION: EXPRESSED IN LIVE, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BLAUR, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 1597
LENGTH: 487
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PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-00-04
PRIOR FILING DATE: 2000-00-04
PRIOR PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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RIOR APPLICATION NUMBER: PCT/US01/00668
RIOR FILING DATE: 2001-01-30
RIOR APPLICATION NUMBER: PCT/US01/00668
RIOR APPLICATION NUMBER: PCT/US01/00663
RIOR APPLICATION NUMBER: PCT/US01/00662
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RIOR REPLICATION NUMBER: PCT/US01/00661
RIOR APPLICATION NUMBER: PCT/US01/00670
RIOR APPLICATION NUMBER: PCT/US01/00670
RIOR APPLICATION NUMBER: US 00/234,687
ROR APPLICATION NUMBER: US 09/608,408
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FILE REFERENCE: Aeomica X-1
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nk, David R.
nzel, David K.
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Search completed: February 29, 2004, 22:23:53
Job time : 211 secs
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US-10-029-386-4279/c
Sequence 4279, Appl:
Publication No. US2
                                                                                                                                         Query Match
Best Local S
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APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

TITLE OF INVENTION: HUWAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR INTERFERENCE: ABOMICA-X-2

CURRENT APPLICATION MUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

FENCIFIC. SAT
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                                                                                                                                                                       OTHER INFORMATION: MAP TO CHR22_81.0
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.46
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.49
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.49
OTHER INFORMATION: SWISSPROT HIT: P46060, EVALUE 1.00e-06
OTHER INFORMATION: EST HUMAN HIT: BE392547.1, EVALUE 5.00e-06
OTHER INFORMATION: NT HIT: 9114779148, EVALUE 8.00e-31
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Best Local Similarity 89.4
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                     LENGTH: 543
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                   1 GAGGATGAAGCTGAAGAGGAGGAGGAAGGAGGAGGAGGAAGA 47
                                                                                                                          42;
                                                                                                                                    Similarity
                                              Conservative
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.US20030194704A1
                                                                                                                               76.5%;
89.4%;
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89.4%;
                                                                                                       Score 39; DB 14; Length 543; Pred. No. 0.024; Indels
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Pred. No. 0.024;
0; Mismatches
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Minimum DB
Maximum DB
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Maximum Match 100%
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SUMMARIES

## Score 46 Query Match 100 1 143350 241678 288697 289758 216505 231171 194614 301817 83802 124474 261258 276543 254400 Length 1344 22842 1168 1180 1197 1050 1183 1183 1180 1185 1185 6904 885 1030 1353 1353 2072 2072 2072 3274 9944 1180 11180 11218 ÐB 10 4 10 5 10 AF366899 MUSADRRECA ALT31836 AC126878 ACC91365 ACC91365 ACC12830 ACRAZBARA 0 EDO427270 0 ASP427259 TTE315939 MSP251185 AC132091 AC102410 AC130635 AC134133 EAT419810 CPO271336 AC092603 PVI251176 LPA505821 LPA315941 AC099140 AC139950 AC103491 AC116220 AC125122 AC132383 AC132385 AY341886 AC121509 AC121484 AC106171 AC133236 AC105607 AC095629 AC132695 AY121768 HAM251178 AY150333 AC113944 AX350489 AR270618 ä RTU419814 OCY16189 AC09557: OCAAR2B AF005900 AX548756 HUMADRA2RA HSA325747 AX348497 RATA2BR AR270618 Sequence M34041 Human alpha AX548756 Sequence AP005900 Homo sapi AJ251186 Nycticebu AJ427266 Trichys f AF3320049 Mus muscul AF332009 Mus muscul AF332009 Mus muscul AF332009 Mus muscul AF332009 Mus muscul AF332001 Rat alpha-2 AF366899 Rattus no M94533 Mus muscul AC1226878 Rattus no AC122830 Rattus no AC112830 Rattus no AC127136 Cavia por AJ419811 Ribgeessa Y15945 Equus cabal AY15033 Tupaia be AC1123944 Mus muscu AC123148 Hippopota AJ42770 Erethizon AJ42770 Erethizon AJ42770 Erethizon AJ42773 Rattus no AC12169 Mus muscu AC12169 Mus muscu AC12169 Mus muscu AC12169 Rattus no AC12169 Rattus no AC12169 Rattus no AC13269 Rattus no AX350490 Sequence AF316895 Homo sapi AC092603 Homo sapi AJ251176 Phoca vit AJ325747 Homo sapi AX350489 Sequence AX348497 Sequence M38742 Human alpha AJ505821 Lama paco AJ315941 Lama paco Description AX344976 Sequence S67319 alpha 2-adr S67316 alpha 2-adr

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RESULT 2 S67316 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	Query Match Best Local Matches 5 Qy 1 Db 13	gene ORIGIN ,	AUTHORS TITLE JOURNAL MEDLINE PUBMED REMARK FEATURES SOUTCE	RESULT 1 S67317S2 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SEGMENT SOURCE ORGANISM REFERENCE	139 C 140 C 141 C 143 C 144 C 145 C 147 C 147 C 147 C 149
E E E	Whatch 100.0%; Score 51; DB 10; Length 246; Local Similarity 100.0%; Pred. No. 7.4e-05; 1es 51; Conservative 0; Mismatches 0; Indels 0; Gaps 1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGAGAGTGTGAACCCCAG 51	/organism="Rattus sp." /mol_type="maNA" /db_xref="taxon:10118" order(867317.1:1130,1246) /gene="alpha 2-adrenergic receptor"	Wang, S.Y. Identific 2-adrener, Diabetes 94085695 8262309 GenBank st entry [NCE This seque	3 %	35 68.6 204175 2 AC128278 35 68.6 206497 10 AC094389 35 68.6 210680 2 AC123724 35 68.6 210680 2 AC123724 35 68.6 214572 10 AL450341 35 68.6 215642 2 AC117634 35 68.6 216386 2 AC117634 35 68.6 216531 2 AC111957 35 68.6 227366 2 AC11957 36 68.6 227366 2 AC118100 35 68.6 227366 2 AC118100 36 68.6 237366 2 AC199091 36 68.6 237368 2 AC199091 37 68.6 237368 2 AC19588 38 68.6 237368 2 AC19588 39 68.6 237368 2 AC119588 30 68.6 237365 2 AC119588 31 68.6 237365 2 AC119588 32 68.6 237365 2 AC119588 33 68.6 237365 2 AC115293 34 AC115293 AC115293 Mus muscu

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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 1344)

Small, K.M., Brown, K.M., Forbes, S.L. and Liggett, S.B.
Polymorphic deletion of three intracellular acidic residues of the alpha 2B-adrenergic receptor decreases G protein-coupled receptor kinase-mediated phosphorylation and desensitization J. Biol. Chem. 276 (7), 4917-4922 (2001)
                                   Homo sapiens BAC clone
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AC092603.2 GI:16303539
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LCAISLDRYMAVSRALESYNSKRTFRRIKCIILTYWLIALVISLPPLIYKGDQSPQDRG
RPQCKLNQBAWYILASSIGSFBAPCLIMILVYLRIYLLAKRSMRRGBRAKGGPQGES
KQPRPDHGGALASAKLPALASVASAREVNGHSKSTGEKEEGETPEDTGTRALPPSWAA
LPNGGQGKEGVCGASPEDDALEEEEEEEECEGPAVPYSPASACSPPLQOPQGSRVAA
LLNGGQGVLGGGWGRRRAQITREKRFTFVLAVVIGVPVLCWFPFFSYSLGA
                                                                                                                                                                                                                                                                                                                                                                                 /note="compared to wild type sequence presented in G
Accession Number AF005900; polymorphic sequence lack
three glu residues at this location"
/frequency="Caucasians 0.31; African-Americans 0.12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  891^892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="alpha_2B_adrenergic_receptor"
/protein_id="AAK01635.1"
/db_xref="GI:12698670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="ADRA2B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="ADRA2B"
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/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                 replace="gaagaggag"
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                                       GI:16303539
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_xref="taxon:9606"
                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                  Score 51; DB
Pred. No. 7e-
0; Mismatches
                                                                           22842 bp
RP11-139J6
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7e-05;
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                                                                           linear
complete
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                                                                           sequence
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lacks
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SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, B., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
                                                                                                                                                                           MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Oct 20, 2001 this sequence version replaced gi:14916188.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (23-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
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5 (bases 1 to 22842)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (20-OCT-2001) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (19-UUL-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. 4 (bases 1 to 22842)
Waterston, R. H.
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The sequence of Homo sapiens
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manmalla; Eutheria; Chordata; Craniata; Manmalla; Eutheria; Primates; Catarrhini l (bases I to 22842) Sulston, J. E. and Waterston, R. Toward a complete human genome sequence genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
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piens BAC clone RP11-139J6
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4444 Forest Park Parkway, St.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone sequenced to the left is RP11-401C13, 2000 bp overlap; the clone sequenced to the right is RP11-574O17, 2000 bp overlap. Actual end of this clone is at base position 48999 of RP11-574O17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphisms have been identified between AC013272 and AC092603.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and coworkers at http://www.chori.org
VECTOR: pBACe3.6
                                                                                                                                                                                                       /rpt
12062
                                                         'note="match to EST
                                                                                         note="match to EST AI791589
                                                                                                                                                                    note="match to EST AI733093
                                                                                                                                           note="match
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                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="MIR"
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7278. .7415
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5576. .5870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="(GGCTG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Alu"
5873. .6183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="MIR"
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/mol_type="genomic DNA"
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              EST BF475329
                                                     BF475329
      (NID:g11546156)"
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                                               (NID:g11546156) "
                                                                          (NID:95339305) oj40h05.y5
                                                                                                                   (NID:g3002438) oj40h05.sl"
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Madsen,O.
Direct Sub
Submitted
                                                                                                                                                                                                                                                                           Phoca vitulina partial aar2B
                                                                                                                                                                                                               aar2B gene; alpha adrenergic receptor
Phoca vitulina (harbor seal)
Phoca vitulina
                                                                                                                                       Madsen,O., Scally,M., Douady,C.J., Kao,D.J., DeBry,R.W., Adkins,R., Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
                                                                                                                        Parallel adaptive
                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae;
                                                                                                                                                                                                                                                              AJ251176.1 GI:11322419
                                                                                        Nature 409 (6820), 610-614 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                             1214318
                                                                                                                                                                                                                                                                                                                                                                                      GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCCAG 51
                                             (bases 1 to 1168)
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                Submission
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14762. 14822
/note="similar to Homo sapiens E/
(NID:g12877089)"
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15110. .15648
/note="similar to Rattus norvegicus EST AW916723
(NID:g8082456)"
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/note="CpG_island (%GC=74.2,
14900. .15218
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(18-NOV-1999) Madsen O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="match to EST AA836522 (NID:g2910841) od22d08.s1"
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/note="match to EST AA830781 (NID:g2903880) oc56b01.sl"
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(NID:912877089)"
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                                                                                                                        radiations in two major
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Pred. No. 6.3e-05;
Pred. No. 6.3e-05;
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Department of Biochemistry,
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SOURCE
ORGANISM
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Molecular ev
Unpublished
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                                                                                                                                                                                                                                                                                                                         Molecular evolution of the mammalian alpha 2B adrenergic receptor Mol. Biol. Evol. 19 (12), 2150-2160 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lama pacos partial adra2b gene adra2b-2 allele.
                                                                                                                                                                    Submitted (14-AUG-2002) Madsen O., 161 Bio of Nijmegen, PO.BOX 9101, 6500HB Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Lama pacos (alpaca)
Lama pacos
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adra2b gene; alpha 2B a
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                                                                                                                                                                                                                                                                                                            L2446807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="Sptrembl:Q9GL07"
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                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                               evolution
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ne alpha 2B a
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ijmegen, NETHERLANDS
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MAM 12-DEC-2002

U. and de receptor

Jong, W.W.

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Query Match
Best Local Similarity 90.2
46; Conservative
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Location/Qualifiers
1. .1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy, W.J., Eizirik, E., O'Brien, S.J., Madsen, O., Scally, M., Douady, C.J., Teeling, E., Ryder, O.A., Stanhope, M.J., de Jong, W.W. Resolution of the early placental mammal radiation using Bayesian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     845 GAGGAGGAGGCTGCAGAGGAGGAGGAGGAAGGAAGAGTGTGAGCCTCAG 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lana pacos partial adrazb gene for alpha 28 AJ315941.1 GI:21212927 adrazb gene; alpha 28 adrenergic receptor. Lana pacos (alpaca)
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/ L'ARBIEL LONE "ALAVITELIL FTI FGNALVILAVLTSRSLRAPQNLELVSLAAA |
RALEYNSKRTPRRIKCI ILTVMLIAVLTSLPLI YKGOQSPQTRGRPQKLKAVS |
LASSIGSFFAPCLIMILTVLTR YLLAKSHRRGFRKAGFGKADSKQPCRIPGEVSAS |
GKLPTLVSQLATAGEANGRPPTGEKDEGETPEDPGTFALEPNMFALPNSGGQKEGV |
CCTSPEEEDALEEECAEEEEEEEEEEEPQALPASPASACSPPLQQPQLSRVLATLRCQV |
LLGRGVCTSRGQMWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPEHC
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GTSRGQWWRRRAQLTREKKFTFVLAVVIGVFVLCWFPFFSYSLGAICPEHCKVPRGL
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                                                                                                                                                                                                                                                                                                                          'gene="adra2b"
                                                                                                                                                                                                                                                                                                                                                         mol_type="genomic DNA
db_xref="taxon:30538"
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mol_type="genomic DNA"
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Pred. No. 0.014;
0; Mismatches
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Best Local Similarity 90.2
Matches 46; Conservative
1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGTGTGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5880 GAGGATGAAGTTGAAGAGGAGGAGGAAGGAAGAATTGTGAA 5924
                                                                     43;
                                                          Similarity 95.6
43; Conservative
                                                                                                                                                                                                                                                                   Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of behavioural disorders, neurological disorders
                                                                                                                                                                                                                                             Epigenomics AG
                                                                                                                                                                                                                                                 Patent: WO 0202809-A 5 10-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                       synthetic construct
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Sequence 5 from Patent WO0202809.
AX348497
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Sequence 47 from Patent
AX344976
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                                                                       82.0%;
95.6%;
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95.6%;
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90.2%;
                                                 Score 41.8; DB
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PUBMED REFERENCE AUTHORS TITLE

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JOURNAL MEDLINE

TITLE AUTHORS

REFERENCE

SOURCE DEFINITION ACCESSION VERSION

ORGANISM

RESULT 8 LPA315941

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PAT 06-FEB-2002

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5880 GAĞGATGAAĞTTGAAĞAĞGAĞGAĞĞAĞĞAĞĞAAĞATTĞTĞAA 5924

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Length 6904; Indels

<u>,</u>

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REFERENCE
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HSA325747/c
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HUMA2C2
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Best Local S
Matches 44
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Original source text: Human adult ne Draft entry and computer-readable se kindly gubmitted by A.C.Chang, 20-SEP-1990.
Institute of Neuroscience 155, Sect II, Li-Noon St.
Taipei, Taiwan, 1121 ROC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                             610
                                                                                                                                                                                                                                                                                                                                                4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGAGAGTGTGAACCCCAG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 885)
Chang, A.C., Ho, T.F. and Chang, N.C.
Chang, A.C., Ho, T.F. and Chang, N.C.
In vitro amplification by polymerase chain reaction of a partial
gene encoding the third subtype of alpha-2 adrenergic receptor in
                                                                                 Homo sapiens
NB1-818S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys.
91054503
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alpha-2 adrenergic receptor.
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AJ325747.1
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                              HSA325747
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/product="alpha-2-adrenergic receptor"
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/protein_id="alpha-2-adrenergic receptor"
/protein_id="alpha-2-adrenergic receptor"
/db_xref="GDI:GO0-120-540"
/db_xref="GDI:GO0-120-540"
/db_xref="GDI:GO0-120-540"
/db_xref="GDI:GO0-120-540"
/db_xref="GI:177868"
/db_xref="GI:17
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/db_xref="taxon:9606"
/map="4p16.3-p15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="ADRA2C"
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mol_type="genomic DNA"
                                                                                                             genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     81.6%;
91.7%;
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_type="neuroblastoma"
ue_type="neural"
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                                                                                                                                              1030 bp
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receptor
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sequence for [
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AX350489
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1 (bases 1 to 1030)

Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M., Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V., Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I., Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R. Nott lanking sequences: a tool for gene discovery and verification
                                                                                                                                                                                                                                                                                                                                                                                                                                              1353 bp
Sequence 1 from Patent WO0179561.
AX350489
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                                                                                                                          44;
                                                                                                                                                                                                                                                                          Alpha-2 adrenergic receptor polymorphisms Patent: WO 0179561-A 1 25-OCT-2001; Liggett, Stephen B. (US); Small, Kersten
                                                                                                                                                                                                                                                                                                          Liggett, S.B. and Small, K.M. Alpha-2 adrenergic recentor
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Zabarovsky, E.R.
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llarity 91.7%;
Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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91.7%;
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Box 280, Stockholm 171 77,
                                                                                                                                                     Length 1353;
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LOCUS DEFINITION

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1181

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2072 patent US

6500938.

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10-APR-2003

ACCESSION VERSION KEYWORDS

SOURCE

ORGANISM

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Length 2072; Indels

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.. 1 (bases 1 to 2072)
Lomasney,J.W., Lorenz,W., Allen,L.F., King,K., Regan,J.W., Yang-Feng,T.L., Caron,M.G. and Lefkowitz,R., Expansion of the alpha 2-adrenergic receptor family: cloning and characterization of a human alpha 2-adrenergic receptor subtype, Proc. Natl. Acad. Sci. U.S.A. 87 (13), 5094-5098 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Original source text: Human placenta DNA, clone alpha-2 C2.
Draft entry and computer-readable sequence for [1] kindly submitted
by J.W.Lomasney, 03-MAY-1990, for release after publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha-2-adrenergic receptor; plasma membrane protein; receptor-coupled G protein.
Homo sapiens (human)
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                                        /GOUGH.BUGGER / GOOGH 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.

1 (bases 1 to 2072)
Au-Young, J. and Seilhamer, J.J.
Composition for the detection of signaling pathway gene expression
Patent: US 6500938-A 1181 31-DEC-2002;
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AR270618.1
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alpha-2-adrenergic receptor (alpha-2
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ilarity 91.7%;
Conservative
                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                         name 'ADRA2RL1'"
                                                                                                                                                                                                                                                                                                                                    note="alpha-2-adrenergic receptor (alpha-2 C2)
                                                                                                                                                                                                                                                                                                                                                                                    /gene="ADRA2B"
                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ADRA2B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xref="taxon:9606"
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Pred. No. 0
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AX548756
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Best Local !
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                                        CHU Rangueil, Toulouse 31403, France
3 (bases 1 to 9944)
Cayla, C., Heinonen, P., Viikari, L., Schaak, S., Snapi
Bouloumie, A., Karvonen, M., Pesonen, U., Scheinin, M.
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                                                                                                                                    Direct Submission
Submitted (29-MAY-1997) INSERM Unit 317,
                                                                                                                                                                             2 (bases 1 to 9944)
Cayla, C., Schaak, S., Bouloumie, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       892
                                                                                                                                                                                                                                                                    Cayla, C., Heinonen, P., Viikari, L., Sch.
Bouloumie, A., Karvonen, M., Pesonen, U.,
                                                                                                                                                                                                                                                      Alpha2C2-adrenergic receptor
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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complete cds. AF005900
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Pattent: WO 02061087-A 41 08-AUG-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burmer,G.C., Roush,C.L. and Brown,J.P.
Antigenic peptides, such as for G protein-coupled receptors
(GPCRs), antibodies thereto, and systems for identifying such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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44; Conservative
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(05-AUG-2003) INSERM Unit 317, Institut Louis
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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U., Scheinin,M. and Paris,H.
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PRI 05-AUG-2003

Institut Louis Bugnard

Snapir, A

and Paris, H.

Bugnard,

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                                                                                                                                                                                                                                                                   Madsen,O., Scally,M., Douady,C.J., Kao,D.J., DeBry,R.W., Adki.
Amrine,H.M., Stanhope,M.J., de Jong,W.W. and Springer,M.S.
Parallel adaptive radiations in two major clades of placental
                                                                                                                                                                                                                                                                                                                                   Nycticebus coucang
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Strepsirhini; Loridae; Nycticebus.
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Sequence update by submitter
On Aug 5, 2003 this sequence version
Location/Qualifiers
                                                                                                           Submitted (18-NOV-1999)
University of Nijmegen,
                                                                                                                                                                                                                                                                                                                                                                                                            AJ251186.1 GI:11322429
Bar2B gene; alpha adrenergic receptor
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                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                    Nature 409 (6820), 610-614 (2001)
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                                                                                                                                                                                   (bases 1 to 1180)
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/organism="Nycticebus coucang"
/mol_type="genomic DNA"
/db_xref="taxon:9470"
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VLATLRGQVLLGRGVGAIGGQWWRRRAQLTREKRFTFVLAVVIGVFVLCWFPFFFSYS
LGAICPKHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRPWTQTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="alpha28-adrenergic receptor"
/protein_id="AAB62558.1"
/db_xref="61:2245628"
                                                                            Location/Qualifiers
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/note="alpha2C2 ad
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/db_xref="taxon:9606"
/chromosome="2"
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mol_type="genomic DNA"
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                                                                                                               Madsen O., Department of Biochemistry, P.O. box 9101, 6500 HB Nijmegen,
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adrenergic receptor
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                                                            CDS
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KEYWORDS
SOURCE '
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                            J (bases 1 to 1218)
Douzery, E.J. P.
Direct Sub-
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AZAB gene; alpha 2B adrenergic receptor.
Thomomys talpoides (northern pocket gopher)
Thomomys talpoides
Thomomys talpoides
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Rodentia; Sciurognathi; Geomyidae;
                                                                                                                                                                                                                                                                                                                                                  Submitted (04-JAN-2002) Douzery E.J.P., Institut des Sciences (l'Evolution, Lab. Paleonto., Paleobio., Phylogenie, Universite Montpellier II, Pl. E. Bataillon, 34 095 Montpellier Cedex 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huchon,D., Madsen,O., Sibbald,M.J., Ament,K., Stanhope,M.J., Catzeflis,F., de Jong,W.W. and Douzery,E.J.
Rodent phylogeny and a timescale for the evolution of Glires: evidence from an extensive taxon sampling using three nuclear Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Douzery, E.J.P., Delsuc, F., Stanhope, M.J. and Huchon, D. Local molecular clocks in three nuclear genes: divergence rodents and other mammals, and incompatibility among fossi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor, exon
AJ427262
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Thomomys talpoides partial A2AB
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RALEYNSKRTPRRIKCIILTVMLIAAVISLPFLIYKGGFGKGSSKQPQPVPGGALAS
RAPTPASALASAGEANGCSKPPGEKEEGETLEDVGSRPLPFGWAALSNSGQGKEGV
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GAVGGQWWRRRAQLSREKRFTFVLAVVIGVFVLCWFPFFFSYSLGAICPKHCKVPHGL
F"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/product="alpha 2B adrenergic receptor"
/protein_id="CAD20300.1"
                                                                                                                                                                                                                      /organism="Thomomys talpoides"
/mol_type="genomic DNA"
                                                                                                                                                                                     db_xref="taxon:35660"
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                                                                                                                                         /gene="A2AB"
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88.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene for alpha 2B adrenergic
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fossil
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Submitted (04-JAN-2002) Douzery E.J.P., Institut des Sciences de l'Evolution, Lab. Paleonto., Paleobio., Phylogenie, Universite Montpellier II, Pl. E. Bataillon, 34 095 Montpellier Cedex 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Mol. Evol. (2003) In press
3 (bases 1 to 1179)
Douzery,E.J.P.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Douzery,E.J.P., Delsuc,F., Stanhope,M.J. and Huchon,D.
Local molecular clocks in three nuclear genes: divergence times
rodents and other mammals, and incompatibility among fossil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huchon,D., Madsen,O., Sibbald,M.J., Ament,K., Stanhope,M.J., Catzeflis,F., de Jong,W.W. and Douzery,E.J.

Rodent phylogeny and a timescale for the evolution of Glires:
evidence from an extensive taxon sampling using three nuclear genes
Mol. Biol. Evol. 19 (7), 1053-1065 (2002)
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Trichye fasciculata (long-tailed porcupine)
Trichye fasciculata
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Hystricidae; Trichys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trichys fasciculata partial A2AB
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/db_xref="GOA:88KIP2"
                                  db_xref="SPTREMBL:Q8K1P2"
                                                                                                                                                                                                                                                                                                                                                                                                organism="Trichys fasciculata"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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SAKVQTLASHLSSIGEANGHPNPPGEKEEGDTPEDSGARALPSWALLBNSGQGKKK
SAKVQTLASHLSSIGEANGHPNPPGEKEEGDTPEDSGARALPSWALLBNSGQGKKK
ATLRGQVLLGKGYGAISGQWWRRRTQLTREKRFTFVLAVVJGVFVLCWFPFFFSYSLG
ATTAGQVLLGKGYGAISGQWWRRRTQLTREKRFTFVLAVVJGVFVLCWFPFFFSYSLG
                                                                                                                                                                                                                                                                                                                                             xref="taxon:73865"
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Pred. No. 0.041;
0; Mismatches 6;
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gene for alpha 2B adrenergic
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REFERENCE
Query' Match
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AUTHORS
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ORGANISM
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VERSION
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LOCUS
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehringer, M.A., Thompson, J., Conroy, O., Xu, Y., Yang, F., Canniff, J., Beeson, M., Gordon, L., Bennett, B., Johnson, T.E. and Sikela, J.M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ehringer, M.A., Thompson, J., Conroy, O., Xu, Y., Yang, F., Beeson, M., Gordon, L., Bennett, B., Johnson, T. E. and Sike High-throughput sequence identification of gene coding within alcohol-related QTLs Mamm. Genome 12 (8), 657-663 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 1347)

Conrov.O., Xu,Y., Yang,F., Canniff,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44;
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                                                   /gene-madra2b"
/gene-madra2b"
/codon_start=1
/codon_start=1
/product=-madrenergic_receptor_alpha_2B"
/product=-madrenergic_receptor_alpha_2B"
/product=-madrenergic_receptor_alpha_2B"
/product=-madrenergic_receptor_alpha_2B"
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/product=-madrenergic_receptor_alpha_2B"
/db_xref=-madrenergic_receptor_alpha_2B"
/db_xref=-madrenergic_receptor_alpha_2B"
/cranslation=-myHogerysvoyalalpha_2B"
/cranslation=-myHoger
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                                            AICPOHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRQWTQTGW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="Adra2b"
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/gene="A2AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _type="mRNA"
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86.3%;
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Pred. No. 0.12;
0; Mismatches 7;
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Xu,Y., Yang,F., Canniff,J., son,T.E. and Sikela,J.M.

JOURNAL REFERENCE AUTHORS TITLE

calibrations
J. Mol. Evol.
3 (bases 1 for

JOURNAL

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE

REFERENCE AUTHORS

TITLE

KEYWORDS SOURCE

ORGANISM

VERSION ACCESSION DEFINITION

AJ427266.1 GI:21665899

RESULT 20 TFA427266 LOCUS

TFA427266

1347 bp

linear

2B

ROD 21-FEB-2002 B (Adra2b) mRNA,

Indels Length 1179;

0,

Gaps

0

뭐 Ś

883

ORIGIN

exon

/gene="A2AB"

Query Match
Best Local Similarity 88.2

81.2%; 88.2%;

.,

FEATURES

source

gene CDS

B

gene="A2AB" gene="A2AB"

76.1%; Score 38.8;

DB 10;

Length 1347;

L00979.1 GI:191547

2-C2

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RESULT 23
MUSAADRENH
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Mus musculus
complete cds.
AF332050
                                                                                                                                                   1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGATGTGAACCCCA
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                               MUSAADRENH
Mus musculus alpha-2
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Sciences (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1347)
Ehringer, M.A., Thompson, J., Conroy, O., Xu, Y.,
Beeson, M., Gordon, L., Bennett, B., Johnson, T.E.
complete cds.
L00979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High-throughput sequence identification within alcohol-related QTLs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehringer, M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MU8
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                                                                                                                                  GAGAAGGAGCTGAAGAGGATGAAGAGGAGGTGGAAGAATGTGAACCCCCA
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Center, 4200 East Ninth Ave C236, Denver, CO 80262, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                               /translation="MVHQEPYSVQATAAIASAITFLILFTIFGNALVILAVLTSRSLR
APQNLFLVSLAADILVATLIIPSLANGLLGYWYFWRAWCEVULALDVLFCTSSIVH
LCAISLDRYMAVSRALEWSKRTPRRIKCIILTVWLIALDVISJEDLYKGDQREEHG
LPQCELNQEAWYILASSIGSFFAPCLIMILVYLRIYVIAKRSHCRGLGAKRGSGEGES
KKPHPAAGGVPASAKVPTLVSPLSSVGEANGHPKAPPREKEEGEFFEDPEARALPPNWS
ALPRSVQDQKKGTSGATAEKGAEEDDEEEVEECEPQTLPASPASVFNPPLQQPQTSRVL
ATLRGQVLLSKNVGVASGQWWRRRTQLSREKRFTFVLAVVIGVEVVCWPPPFFFSYSLG
AICPQHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRQWTQTGW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol
                                                                                                                                                                                                                                                                                                                                                                                                                     /product="adrenergic receptor alpha 28"
/protein_id="AAK56079.1"
/db_xref="GI:14193668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Adra2b"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="Adra2b"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
|mol_type="mRNA"
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86.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             657-663 (2001)
                               adrenergic
                                                                                                                                                                                               Score 38.8; DB Pred. No. 0.23; 0; Mismatches
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0; Mismatches
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                                                1650 bp
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                               DNA linear ROD 27-
receptor (Malpha2-2H) gene,
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. and Sikela, J.
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                                                  ROD 27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROD 21-FEB-2002
3 (Adra2b) mRNA,
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92378586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
                                                                                                                 Original source text: Rat (strain cDNA to mRNA, clones dz-(3,5,6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCA
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                                                                                 Draft entry and computer-readable K.R.Lynch, 12-FEB-1990.
                                                                                                                                                                                 Molecular characterization of a rat alpha 2B-adrenergic Proc. Natl. Acad. Sci. U.S.A. 87 (8), 3102-3106 (1990)
                                                                                                                                                                                                                  1 (bases 1 to 2319)
Zeng,D.W., Harrison,J.K.,
Lu,Z.H. and Lynch,K.R.
                                                                                                                                                                                                                                                                                   Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                     adrenergic receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                         RATA2BR
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                                                                                                                                                   2158103
                                                                                                                                                                                                                                                                     Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                     Rat alpha-2B-adrenergic
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                                                                                .R.Lynch,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MVHQEPYSVQATAAIASAITFLILPTIFGNALVILAVLTSRSLR
APQNLFLVSLAAADILVATLIIPTSLRAKETYVLALDVLFCTSSIVH
LCAISLBRYMAVSBALESVUSKTPRELKCIILTVWLIAAVLTSLPPLTYKGDQREEPHG
LPQCELNQEAWYILASSIGSFPAPCLIMILVYLRIYVIAKRSHCRGLGAKRGSGEGES
KCRRDAAGGVPASAKVPTLVSPLSSVGEANGHPKPPREKEEGETPEDPEARALPPNWS
ALPRSVQDQKKGTSGATAEKGAEEDEEEVEECEPQTLPAFBASVFNPPLQQPQTSRVL
ATLRGQVLLSKNVGVASGQWWRRRTQLSREKRETFVLAVVIGVEVVCWFPFFFSYSLG
AICPQHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRQWTQTGW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source text: Mus musculus Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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/protein_id="AAA37131.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mol_type="genomic DNA"
strain="129/Sv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                    .2319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.1%;
86.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38.8; DB Pred. No. 0.23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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                                                                                                                                                                                                                                                                                                                                                                                                     2319 bp
receptor
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                                                                                                                                                                                                                                  D'Angelo, D.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Daunt, D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186
                                                                                                                                                                                                                                                                                                                                                                                                     mRNA linear
(RNG-alpha-2) mRNA,
                                                                                                    sequence
                                                                                                                                Sprague Dawley) adult kidney,
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                                                                                                                                                                                                                                    Barber, C.M.,
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                                                                                                   [1] kindly submitted
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/sex="male"

SgS

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1 (bases 1 to 6268)
Schaak,S., Cussac,D. and Paris,H.
Cloning and characterization of the rat alpha2B-adrenergic receptor
                                                                                                                                                                                                                                                                                                    Submitted (29-MAR-2001) U388,
                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 6268)
Schaak, S., Cussac, D. and Paris, H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus alpha2B-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGATGTGAACCCCA 50
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                                  /product="alpha2B-adrenergic receptor"
2408. 2779
/gene="Rng"
/note="5'UTR"
                                                                                                                                                                                              /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSGPTMDHORPYSVQATAAIASAITFLILFTIFGNALVIIAVIT
SRSLRAPONLFLVSLAAADILVATLIIPFSLANELLGYWYFWRAWCEVYLALDVLFCT
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PARGLPCCELNQEAWYILASSIGSFFAPCLIMILVYLRIYVIKARSHCRGLGAKRGS
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TERVLATLRSGCOOKKCTSGATAEEGDEEDEEVEECGETLAVVIGVFVVCWFPFFF
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SYSLGAICFQHCKVPHGLFQFFFWIGYCNSSLNPVIYTVFNQDFRRAFRRILCRPWTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="RNG-alpha-2"
/note="there is no consensus sequence for N-linked 91yosylation (NXS/T) in this receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="kidney"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="RNG-alpha-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:10116"
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Pred. No. 0.22
0; Mismatches
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Sciurognathi; Muridae;
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.22;
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; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene,
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                                                                                    REFERENCE
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MEDLINE
PUBMED
REFERENCE
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AUTHORS
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TITLE
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SOURCE
ORGANISM
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MUSADRRECA
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ACCESSION
                        REMARK
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Best Local Similarity
Matches 43; Conserv
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Chang,A.C.
Chang,A.C.
Direct Submission
Submitted (24-MAY-2002) Neuroscience, National Yang-Ming
University, 155, sect. II, Li-Noon St., Taipei, Taiwan 112,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3677
                                                                                                                       3 (bases 1 to 9377)
Chang,A.C.
Direct Submission
Submitted (27-APR-1993) Neuroscience, National Yang-Ming
University, 155, sect. II, Li-Noon St., Taipei, Taiwan 112,
                                                                                                                                                                                                                                      2 (bases 1 to 9377)
Chen,W.M., Chang,A.C., Wang,C.M., Lin,C.C.
Characterization of the regulatory regions
adrenoceptor subtype gene
Neurosci. Lett. 210 (1), 33-36 (1996)
                                                                                                                                                                                                                                                                                                                                             adrenoceptor subtype gene
Biochim. Biophys. Acta 1171 (2), 219-223 (1992)
                                                                                                                                                                                                                                                                                                                                                                    Chen, W.M., Chang, A.C., Shie, B.J., Chang, Y.H. and Chang, N.C. Molecular cloning and characterization of a mouse alpha 2C2
                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 9377)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           alpha-2 adrenergic receptor. Mus musculus (house mouse) Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUSADRRECA 9377 bp
Mus musculus alpha-2C2 adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGTGTGAACCCCA 50
                                                                                                        (bases 1 to 9377)
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/gene="Rng"
/note="3'UTR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="Rng"
/note="polyA_signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="polyA_site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="Rng"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Codon_start=1
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/db_xref="di:14039789"
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86.08;
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Pred. No. 0.22;
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of m
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murine alpha 2C2
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; Murinae; Mus.
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JOURNAL REFERENCE AUTHORS TITLE

gene promoter Unpublished

FEATURES

France

source

mRNA 5'UTR

> gene="Rng" /gene="Rng" 2408. .5989 'gene="Rng"

gene promoter

JOURNAL

REFERENCE AUTHORS

Rattus

TITLE

SOURCE ORGANISM

CEYWORDS

ACCESSION VERSION

AF366899 AF366899.1

GI:14039788

RESULT 25 AF366899 LOCUS

밁 δ

1263

ORIGIN

Query Match Best Local Similarity

Matches

43;

76.1%; llarity 86.0%; Conservative

DEFINITION

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REFERENCE
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ORIGIN
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AL731836
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Best Local Similarity
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Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 30, 2002 this sequence version replaced gi:21104241.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeates; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6161 GAGAAGGGAGCTGAAGAGGATGAAGAGGAGGTGGAAGAATGTGAACCCCA 6210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>۵</u>
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AL731836.10
HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (28-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse DNA sequence from clone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 83802)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSGPAMVHQEPYSVQATAAIASAITFLILFTIFGNALVILAVLT
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PEPHGLPQCELNQEAWYILASSIGSFFAPCLIMILVYLRIYLIAKRSHCRGLGAKRGS
GEGESKKPRPGPPAGGVPASAKVPTLVSPLSSVGEANGHPKPPREKEEGETPEDPEAR
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8297. .8932
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PQTSRVLATLRGQVLLSKNVGVASGQWWRRRTQLSREKRFTFVLAVVIGVFVVCWFPF
FFSYSLGAICPQHCKVPHGLFQFFFWIGYCNSSLNPVIYTIFNQDFRRAFRRILCRQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="alpha-2C2 adrenergic receptor" 4839. .5257
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/product="alpha-2C2 adrenergic receptor"
/protein_id="AAA73895.1"
/db_xref="GI:927108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:21264639
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86.0%;
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.9377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38.8; DB Pred. No. 0.21;
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n clone RP23-119A13 on chromosome 2, complete
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AUTHORS
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AC126878
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SOURCE
ORGANISM
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                                                                                           Allen, C., Allen, H., Alsbrooks, S., Anina, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Barsalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasax, H., Center, A., Crox, C., Coyle, M., Cree, A., D'Souza, L., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasax, H., Center, A., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chu, J., Clacko, J., Cokreell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., L., Davis, G., Davy, Carroll, L., De Anda, C., Dederich, D., Davila, M., Davis, G., Dava, Carde, A., Garda, C., Dederich, D., Davila, M., Davis, C., Dung, Y., Dinh, H., Divya, K., Depar, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., Farser, C., M., Gabisi, A., Ganta, R., Gardy, M., Guerra, M., Gebregeorgis, B., Geer, K., Gill, R., Gardy, M., Guerra, M., Guevara, M., Gebregeorgis, B., Geer, K., Gill, R., Gardy, M., Guerra, M., Guevara, M., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, J., Hernandez, J., Hulyk, S., Hune, J., Idlebird, D., Jackson, A., Jackson, A., Johnson, R., Johnson, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12506 GAGAAGGGAGCTGAAGAGGATGAAGAGGAGGTGGAAGAATGTGAACCCCCA 12555
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Rattus norvegicus
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus clone CH230-263M16, WORKING DRAFT SEQUENCE, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-119A13 is from the RPCI-23 Mouse PAC_Library
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/db_xref="taxon:10090"
/chromosome="2"
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86.0%;
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Pred. No. 0.
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AL Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

The sequence in this assembly is a combination of BAC based reads (http://www.hgcc.bcm.tmc.edu/projects/rat/). Each contig Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig described individual sequence contigs are ordered and oriented, and separated extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center clone name: CH230-263M16
Assembly program: Phrap; version 0.990329
Consensus quality: 114750 bases at least Q40
Consensus quality: 115674 bases at least Q30
Estimated insert size: 117568; sum-of-contigs estimation

Estimated insert size: 117568; sum-of-contigs estimation
                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Worley,K.C.

Direct Submission
Submitted (10-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 7x in Q20 bases, sum-of-contigs estimation
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AUTHORS
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ORGANISM
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Best Local (
RS Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C. Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C. Barbaria, J., Bencon, J., Bimage, H.C., Are, J.R., Ayele, M., Banks, T., Bouck, J., Bencon, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bencon, J., Birdeva, M., Brown, B., Brown, M., Bryanin, N.P., Carren, F., Carter, M., Carvacos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, Z., Chowdhry, I., Christopoulos, C., Davy-Carroll, L., Dederich, D.A., Delando, C., Davy-Carroll, L., Dederich, D.A., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Edwards, C.C., Elhaj, C., Bscotto, M., Barnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Bscotto, M., Falls, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, C., Harris, K., Harri, M., Havlak, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Harri, M., Havlak, P., Hale, S., Hamilton, K., Homesi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jacobson, B., Jis, Y., Johnson, R., Jolivet, S., Joudah, S., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.C., Liu, J., Liu, M., Loulseged, H., Maheshwari, M., Mapua, P., Martin, R., Martin-R., Martin-R., Martin-R., Ma, J., Ma, J., Man, J., M
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Eukarvora
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC091365.5 GI:23664882
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14 unordered pieces.
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122714 . 124474
/notes"wgs_end_extension
clone_end:Sp6"_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_end:Sp6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end_sequence:BZ271225"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.1%; Score 38.8; Di 86.0%; Pred. No. 0.2;
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922. .122663
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ne CH230-1A10,
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Center: Baylor

----- Genome Center

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

Direct Submission

Rat Genome Sequencing Consortium.

TITLE JOURNAL REFERENCE

(bases 1 to 124474)

JOURNAL AUTHORS

FEATURES

53391

53491

1 53390: contig of 53390 bp in length 53490: gap of unknown length 124474: contig of 70984 bp in length Location/Qualifiers

Bource

TITLE JOURNAL REFERENCE AUTHORS TITLE

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

JOURNAL

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Submitted (10-CCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 10, 2002 this sequence version replaced gi:21953942.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Okwoonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pideas, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, J., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparke, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, T., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Walliamson, A., Wacze, R., Wooden, S., Wolfer, S., Wulliamson, A., Wleczyk, R., Woden, S., Wolfer, K., Wu, Y., F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-APR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 261258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                 NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
                                                                                            as soon as it is available and be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 261258)
                                                                                                                                                                                                                                                                                                                                                  Center project name: TUEV
Center clone name: CH230-1A10
Center clone name: CH230-1A10
Center clone name: CH230-1A10
Center clone name: CH230-1A10
Center clone name: Phrap; version 0.990329
Consensus quality: 190889 bases at least Q40
Centersus quality: 198612 bases at least Q30
Centersus quality: 203158 bases at least Q20
Estimated insert size: 183632; sum-of-centigs estimation
Quality coverage: 5x in Q20 bases; sum-of-centigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: BCM
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    4485
4585
15357
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4484: contig of 4484 bp in length
4584: gap of unknown length
15356: contig of 10772 bp in length
15456: gap of unknown length
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                                              ORIGIN '
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  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                        end_sequence:BH273948"
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                                                                                                                                             note="wgs_end_extension:
lone_end:T7"
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:lone end:T7"
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lone_end:Sp6"
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On Sep 21, 2002 this sequence version replaced gi:21743229.
The sequence in this assembly is a combination of BAC based reads whole genome shotgun sequening reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the contigs that consist entirely of whole genome shotgun sequence contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                        'NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) (NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence that soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-FEB-2002) Human Genome of Molecular and Human Genetics, Bayl Baylor Plaza, Houston, TX 77030, USA 3 (bases 1_to 276543)
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Rat Genome Sequencing Consortium.
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                                                                ane expression profile; hepatotoxicity; liver; toxicity assay; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
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96597
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AAD285551

AAD285551

AAD283583

ABT43588

ABT43588

ABT43588

ABT43586

ADC17326

ADC17326

ADC17326

ADC2916

ABA465987

AAI46158

ABA48106

AAK40143

AAK40143

AAK40143

AAK40143

AAK40143

AAK40143

AAK40143

AAK11411

ABA339726

AAI11706625

AAI11706625

AAI1170665

AAK27111

AAK01665

ABA429711

AAK01658

ABS26696

AAK11401665

AAK11401665

AAK11658

ABS26696

AAK11658

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AAK11658

ABS26696

AAK52886

AAK52886
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ADA052807
ADB725407
ADB72548143
AB674515
AAR1549158
AAR22984
AAK22984
ABS48806
ABS48806
ABS48806
ABS48806
ABS48806
ABS48868
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Aak52886
Aak51902
Ade31391
Abk84534
Abk84534
Abk84534
Abk87236
Ada02651
Adb72389
Aab72389
Aab75454
Abv08936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abq88143 Human ost Abq88143 Human ost Ab474515 Human foe Aai54991 Probe #23 Aak49158 Human bra Ab48886 Human liv Abx90780 Murine ge Aai41957 Probe #10 Aak46237 Human bon Aak1957 Probe #10 Aak56237 Human bon Aak26237 Human bon Aak26237 Human liv Aba59521 Human liv Aad28559 Herpes 8i Abt43584 Mouse cla Abt43584 Mouse cla Abt43585 Mouse cla Abt43586 Human ErN Ada83741 Human KCN Abz20404 Oncofoeta Ada106426 Probe #10 Aba65987 Human bre Aai46158 Probe #16 Aba439726 Human bre Ab440144 Human bre Ab440144 Human bre Ab440145 Probe #16 Aba11702 Probe #16 Aba139076 Human bre Ab401655 Probe #16 Aba2377 Human bre Ab401655 Probe #16 Aba2977 Human bre Ab401665 Human bra Aba26696 Human bra Aba26696 Human bra Aba106628 Probe #16 Aba2777 Human bra Ab401668 Human
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8 Probe #16
1 Human nov
8 CONA sequ
6 Human pro
5 Human pol
1 Human oll
1 Human oll
1 Human dia
4 Gene #370
1 Mouse Sta
9 Mouse Sta
9 Mouse Sta
9 DNA encod
5 Human pro
8 Human pro
8 Human pro
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Mouse
Mouse
        RESULT 2
AAI199906
ID AAI9
XX AAI9
XX AAI9
XX AAI9
XX Huma
XX Huma
XX Poly
KW Poly
KW Cenit
KW Phos
XX Phos
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Best Local S
Matches 51
                                                                     Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor; polymorphic site; allelic variant; cardiovascular disease; central nervous system disease; adenylyl cyclase; MAP kinase activity; phosphorylation; inositol phosphate; alpha-2BAR; chromosome 2; ds.
                                                                                                                                                                           Human alpha-2BAR third intracellular loop variant encoding DNA
                                                                                                                                                                                                                                 18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                  AAI99906;
                                                                                                                                                                                                                                                                                                                   AAI99906 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2002; 2
15-MAR-2002; 2
15-MAR-2002; 2
30-DEC-2002; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-689530/65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-JAN-2003; 2003WO-US003194
                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 100.
51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                 ĠĀĠĀŤĠĀĀĠĊŤĠĀĀĠĀĠĀĠĀĠĠĀĠĠĀĠĠĀĀĠĀĠŤĠŤĠŤĢĀĀĊĊĊĊĀĠ 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                828 BP; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 4067; 1156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; 2002US-00060087;
; 2002US-0364045P;
; 2002US-0364055P;
; 2002US-0436643P;
Location/Qualifiers
1. .1344
                                                                                                                                                                                                                                                                                                                 DNA; 1344 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 51; DE
100.0%; Pred. No. 7.6
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; 271 C; 269 G; 140 T; 0 U; 0 Other;
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7.6e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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120 121 122 123 124 125 126 127 127 129 130 131 131 132 133 134 135 136

RESULT 1
ADB59041
ID ADB5
XX ADB5
AC ADB5
XY O4-I
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04-DEC-2003 ADB59041;

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screening;

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RESULT 3
AAD04761
ID AAD0
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AC AAD0
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                                                                                                                                                                                                                                                                                                   The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (1)-(III) by detecting a polymorphic site, comprising; (a) cobtaining a sample having a polymorphic site, comprising; (a) CC or alpha2C or fragment or complement of, and (b) detecting a polymorphic cite comprising nucleotide positions 901-909 of (I), a site comprising CC cytosine or guanine at position 753 of (IIV) or a site comprising (A) CC (gyggcggggcg) or (B) (gyggcggtgag) at positions 961-972 of (III). The CC method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor gene and further used to determine whether an individual is at increased crisk of developing a disease associated with alpha2B, alpha2A or alpha2, comprising detecting a polymorphic site which correlate to disease and combinations of these. In addition, the technique may be used to predict an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. curvaphrine, norepinephrine, condidine, oxymetazoline, guanabenz, CC (UK14304, BHT933 and combinations of these) or antagonist (e.g. vohimbine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and CC combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to adenylyl cyclase, MAP kinase activity, phosphorylation or inositol continuated for a 9 nucleotide polymorphic site found at nucleotides 901-909 of the human alpha-2BAR variant, the sequence is deleted for a 9 nucleotide polymorphic site found at nucleotides 901-909 of the human alpha-2BAR variant, the sequence is that of the third
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                            Query Match
Best Local
                   AAD04761
                                                    AAD04761 standard;
                                                                                                                                                                                                                                                                                                 Sequence 1344 BP; 220 A; 458 C; 400 G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 144-145; 163pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-APR-2000; 2000US-00551744.
10-AUG-2000; 2000US-00636259.
19-OCT-2000; 2000US-00692077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymorphic site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (LIGG/)
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DB; AAM52118.
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SMALL K M.
                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                      GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGAGAGTGTGAACCCCAG 51
                                                                                                                                              GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 930
                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Small KM;
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/product= "alpha-2BAR"
/product= "sequence is deleted for a 9 nucleotide
/note= "sequence is deleted for a 9 nucleotide
polymorphic site found at nucleotides 901-909 of the
wildtype alpha-2BAR protein (AAI99905)"
                                                    DNA; 1344
                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                          0
                                                        ΒP
                                                                                                                                                                                                                                          Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
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                                                                                                                                                                                                                                          7.8e-05;
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RESULT 4
AAD44388
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AAD44388

standard;

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                                                                                                                      The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) variant protein. Alpha2B-AR has a glutamic acid repeat element (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino acids (amino acids 294-311), located in the third intracellular loop of the receptor polypeptide. The variant is obtained by deletion of three glutamates from the Glu repeat (amino acids 307-309). Alpha2B-AR gene is located on chromosome 2. Alpha2-AR mediate many of the physiological effects of the catecholamines, norepinephrine and cepinephrine. An antagonist of alpha2B-adrenoceptor is useful for treating a mammal suffering from vascular contraction of coronary arteries and a coinically expressed as coronary heat disease (CHD), unstable chronic angina pectoris which is clinically expressed as Prinzmetal's variant form or acute myocardial infarction (AMI). Alpha2B-AR gene is used in
                                                         Query Match
Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Snapir A, H
Scheinin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                        New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                                      Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                               arteries.
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                                                                                                                                                   gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000; 2000WO-FI000913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200129082-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JUVA-) JUVANTIA PHARMA LTD OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-300318/31.
DB; AAE00989.
 880
                                                                                                                                                                                                                                                                                                                                                                                                 3; Page 24-26; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha2B-adrenoceptor (alpha2B-AR) variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; ic acid repeat; intracellular loop; chromosome 2; catechol
                                                          49;
                                                                        Similarity
                   GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCCAG
GAGGATGAAGCTGAAGAGGAGGAAGGAGGAGGAGGAGTGTGAACCCCAG 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heinonen P, A
M, Salonen JT,
, Kauhanen J,
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
/product= "Human alpha2B-adrenoceptor (alpha2B-AR)
variant protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                     219 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .1344
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                                                                       93.7%;
96.1%;
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I, Tuomainen T,
Valkonen V;
                                                                                                                      459
                                                          0
                                                                        Score
Pred.
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                                                                                                                      400
                                                          Mismatches
                                                                        47.8;
No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Karvonen M,
T, Lakka TA,
                                                                                                                      266 T; 0 U; 0 Other;
                                                       DB 5;
0.00057;
les 2;
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                                                                                     Length 1344;
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Nyyssoenen
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len K;
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                              51
                                                          Gaps
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AAD44388;

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RESULT 5
ABL32074
ID ABL3
XX ABL3
AC ABL3
XX BL3
XX
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                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 49
       Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                  Human immune system associated gene SEQ ID NO:
                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                            ABL32074 standard; DNA; 6904 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha-2B-adrenoceptor variant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1344 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 24-26; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting a risk of hypertension and targeting treatment in a determining the pattern of alleles encoding a variant alpha-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-FEB-2001; 2001FI-00000323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-FEB-2002; 2002WO-FI000113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JURI-) JURILAB LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
hypertension; hypotensive; variant; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human alpha-2B-adrenoceptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                         980
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DB; AAE26633.
                                                                                                                                                                                                                                                                                                                                      1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                ĠŔĠĠŔŦĠŔŔĠĊŦĠŔŔĠŔĠĠŔĠĠŔĠĠŔĠĠŔĠĠŔĠĠŔĠĠŔĠŦĠŦĠĸĸĊĊĊĸĠ
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                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 A; 459 C; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "Human alpha-2B-adrenoceptor variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                             93.7%;
96.1%;
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                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 47.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                G; 266 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
.00057;
es 2;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1344,
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                                                                                                                                                                                                                                                                                                                                                   51
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                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 6
AAD28364
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                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                22-APR-2002
                                                                                                                                                                                                                                                                                                                                                                   AAD28364;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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Human; cytostatic; anti
adrenergic alpha-1C-reo
behavioural disorder; n
Tourette's syndrome; sm
drug abuse; migraine; d
30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                 02-JUL-2001; 2001WO-EP007540
                                                                                                                      WO200202809-A2
                                                                                                                                                                                                                                                                                                                                                                              AAD28364 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences including eye diseases such as retinopathy, neovascular glaucoma and leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, artematoid arthitis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6904 BP; 1244 A; 314 C; 2303 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 47; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-2001; 2001WO-EP007537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                    chemically treated genomic DNA #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             GAĞGATGAAĞTTĞAAĞAĞGAĞGAĞĞAĞĞAĞĞĞAĞĞAĞATTĞTĞAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                          antidepressant; neuroleptic; nootropic; antiaddictive; C-receptor; cytosine methylation; therapy; alcoholism; er; neurological; psychiatric; cancer; schizophrenia; e; smoking; human immunodeficiency virus dementia;
                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.0%;
95.6%;
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                                                                                                                                                                                                                                                                                                                                                                          6904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41.8; DI
Pred. No. 0.02:
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3042 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 6904;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abnormal (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>,,</u>
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Best Local
17-APR-2000;
10-AUG-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the diagnosis or therapy of behavioural disorders, neurological disorders and cancer, in particular major depressive disorder, Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, drug abuse, alcoholism, personality traits, compulsive gambling, human immunodeficiency virus dementia, migraine, behaviours in schizophrenic and schizoaffective patients, and suicidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPs). The present sequence is human chemically treated genomic DNA
                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                        GenBank Accession AF009500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAI99905 standard; DNA; 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6904 BP; 1244 A; 314 C; 2303 G; 3042 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of a segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
                                                          17-APR-2001;
                                                                                                                        WO200179561-A2
                                                                                                                                                                                                                                                                                                    central nervous system disease; adenylyl cyclase;
phosphorylation; inositol phosphate; alpha-2BAR;
GenBank Accession AF009500; chromosome 2; ds.
                                                                                                                                                                                                                                                                                                                                                 Human; genotyping; alpha-2B; alpha-2A; alpha-2C; adrenergic receptor;
polymorphic site; allelic variant; cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI99905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pretreated DNA of adrenergic alpha-1C-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligomers useful for detecting cyrosine methylations. The pretreated DNA is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 40-44; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to nucleic acids comprising a segment of chemically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EPIG-)
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                                                                                                                                                                                                                                                                          варіепв
                                                                                                                                                                                                                                                                                                                                                                                               alpha-2BAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
 2000US-00551744.
2000US-00636259.
2000US-00692077.
                                                            2001WO-US012575
                                                                                                                                                  /note= "sequence includes a 9 nucleotide polymorphic
at nucleotides 901-909 absent in the alpha-2BAR varia
(AAI99906)"
                                                                                                                                                                                             /*tag= a
/product= "alpha-2BAR"
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 third
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95.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41.8;
Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                   disease;
MAP kinase activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                site
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                                                                                                                                                                                               The invention relates to genotyping an alpha-2B, 2A, or 2C adrenergic CC receptor gene (I)-(III) by detecting a polymorphic site, comprising; (a) CC obtaining a sample having a polymorphic site, comprising; (a) CC or alpha2C or fragment or complement of; and (b) detecting a polymorphic CC or alpha2C or fragment or complement of; and (b) detecting a polymorphic CC site comprising nucleotide positions 901-909 of (I), a site comprising (A) CC (site comprising at positions 901-909 of (II), a site comprising (A) CC (site comprising at positions 961-972 of (III)) The CC method may be used for genotyping an alpha2B, alpha2A or alpha2C receptor CC gene and further used to determine whether an individual is at increased CC risk of developing a disease associated with alpha2B, alpha2A or alpha2, CC comprising detecting a polymorphic site which correlate to disease and CC combinations of these. In addition, the technique may be used to predict CC an individual's response to an alpha2B, alpha2A, or alpha2C agonist (e.g. CC (UK14304, BHT933 and combinations of these) or antagonist (e.g. vohimbine, prazosin, ARC 239, rauwolscine, idazoxan, tolazoline, phentolamine and CC combinations of these) by detecting the polymorphic site and correlating the site to a predetermined response (where the response is correlated to phosphate levels). The present sequence is that of the third CC intracellular loop of the human alpha-2BAR (GenBank Accession AF009500), the sequence includes a 9 nucleotide polymorphic site at nucleotides 901-909, absent in the alpha-2BAR variant (AAI99906)
                                                                                 Matches
                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genotyping an alpha-2B, 2A, or 2C adrenergic receptor gene useful for determining whether an individual is at increased risk of developing a disease associated with the corresponding receptor comprises detecting
                                                                                                                                                                 Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 144; 163pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-611728/70.
P-PSDB; AAM52117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymorphic site.
                                                                                                     Local
892 GAAGAGGAAGAAGAGGAGGAGGAAGAGAGTGTGAACCCCAG
                                                                                 44;
                         4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGGAGGAGTGTGAACCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIGGETT
SMALL K
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SB,
                                                                                 Conservative
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                                                                                                                                                               224 A; 458 C; 405 G; 266 T; 0 U; 0 Other;
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                                                                                                   81.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
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..
                                                                               Score 41.6; D
Pred. No. 0.02
0; Mismatches
                                                                                                                        BB
                                                                                                                      4
                                                                                 4
                                                                                                                      Length 1353;
                                                                                 Indels
939
                                      51
                                                                                 0
                                                                                 Gaps
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AADO4762
Cbs
                                                                    norepinephrine; epinephrine; therapy; vascular contraction; coronary artery; coronary heat disease; CHD; chronic angina acute myocardial infarction; AMI; Prinzmetal's variant; ds.
                                                                                                       Human; cardiant; gene therapy; alpha2B-adrenoceptor; alpha2B-AR; glutamic acid repeat; intracellular loop; chromosome 2; catechol
                                                                                                                                                                    04-JUL-2001
                                                                                                                                                                                            AAD04762;
                                                                                                                                                                                                                  AAD04762 standard; DNA; 1353
                                                                                                                                            Human
                                             sapiens
                                                                                                                                            alpha2B-adrenoceptor (alpha2B-AR)
                                                                                                                                                                    (first
                    Location/Qualifiers
           . 1353
                                                                                                                                                                  entry)
                                                                                                                                                                                                                    BP.
                                                                                                                                            gene
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catecholamine;

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pectoris;

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RESULT 9
AAD44389
ID AAD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a gene encoding human alpha2B-adrenoceptor (alpha2B-AR) protein. Alpha2B-AR has a glutamic acid repeat element cacids (amino acids 298-309) of 12 glutamates, in an acidic stretch of 18 amino cacids (204-311), located in the third intracellular loop of the protein the chiral protein of cated caced on chromosome 2. CC alpha2-AR mediate many of the physiological effects of the cated on chromosome 2. CC catecholamines, norepinephrine and epinephrine. An antagonist of alpha2B-CC contraction of coronary arteries and a disease involving vascular cc contraction of coronary arteries and a disease involving vascular cc contraction of coronary arteries which is clinically expressed as conficulally expressed as Prinzmetal's variant form or acute myocardial cc infarction (AMI). Alpha2B-AR gene is used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 44
                                             WO200266617-A1
                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                 Human; hypertension; alpha-2B-adrenoceptor; AR; antihypertensive;
                                                                                                                                                                                                                                                                                            Human alpha-2B-adrenoceptor gene.
                                                                                                                                                                                                                                                                                                                                                     13-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                  AAD44389;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAD44389 standard; DNA; 1353 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1353 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA molecule encoding variant specific adrenoceptor protein with deletion of specific amino acids located in the third intracellular loop of the polypeptide, for treating vascular contraction of coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Snapir A, H,
Scheinin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-300318/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salonen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JUVA-) JUVANTIA PHARMA LTD OY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-2000; 2000WO-FI000913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200129082-A1
                                                                                                                                                                                               sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG
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                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                              hypotensive; gene;
                                                                                /product=
                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-00422985.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-29; 37pp; English.
                                                                                                                                                                                                                                                                                                                                         entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.6%;
91.7%;
                                                        "Human alpha-2B-adrenoceptor protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alhopuro P,
T, Tuomainen T,
Valkonen V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Karvonen
T, Lakka
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1353;
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Nyyssoenen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           939
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en K;
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RESULT 10
AAQ14:
ID AAQ14:
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XX AAQ14:
XX AAQ14:
XX AAQ14:
XX Human
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Best Local S
Matches 44
                                 WPI; 1991-310087/42.
P-PSDB; AAR14149.
                                                                                                                                                                                                                                 30,-OCT-1989;
                                                                                                                                                                                           30-OCT-1989;
                                                                                                                                                                                                                                                                              01-OCT-1991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1353 BP; 223 A; 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method for detecting a risk of hypertension by determining the pattern of alleles encoding a variant alpha-2B-adrenoceptor (AR) protein. The methods and compositions of the invention are useful for detecting risks and targeting treatment for hypertension. The kit is also useful for selecting for clinical drug trials testing the antihypertensive effect of compounds. The present sequence is human alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 27-29; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting a risk of hypertension and targeting treatment in a subject determining the pattern of alleles encoding a variant alpha-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-667063/71.
P-PSDB; AAE26634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-FEB-2002;
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ilarity 91.7%;
Conservative
                                                                                              Hartig
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0;

Score 41.6; DB, Pred. No. 0.026; 0; Mismatches

6 4.

Length 1353; Indels

51 0;

Gaps

0,

C; 405 G; 266 T; 0 U; 0 Other;

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Isolated DNA encoding
                                                                                               (NEUR-) NEUROGENETIC CORP
                                                                                                                                                                                                                                                                                   Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta; ss.
                                                                                                                                                                                                                                                                                                                   Human alpha 2 beta adrenergic
                                                                                                                                                                                                                                                                                                                                                                                           AAQ14151 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               892 GAAGAGGAGGAAGAAGGAGGAGGAGGAAGAGTGTGAACCCCAG
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                       89US-00428856
                                                                                                                                               89US-00428856
                                                                                                                                                                                                                                      288. .1752
             human
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     adrenergic receptor -
                                                                                                                                                                                                                                                                                                                                                                                           ВÞ
                                                                                                                                                                                                                                                                                                               receptor gene
for detecting nucleic
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AAT59499
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Best Local S
Matches 44
bind to, th
                                        A genomic DNA clone (AAT59499) codes for human alpha-2B adrenergic receptor (AAM1804), a member of the rhodopsin-like signal transducer family. It was isolated from a human spleen genomic library in the lambda vector Charon 28 by screening with a 1.6 kb fragment of the human 5-hydroxytryptamine receptor gene. Plasmid pNGC-alpha-2B comprising DNA encoding the alpha-2B adrenoceptor is deposited as ATCC 68144. Vectors have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Ltk- cells, designated L-NGC-alpha-2B, are deposited as ATCC CRL 10275. Membranes of such cells can used in novel methods to identify drugs which specifically interact with, and
                                                                                                                                                                                                                                                                                             Disclosure; Fig 2A-E; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-1989;
30-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human alpha-2b adrenergic receptor genomic DNA clone.
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06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2064 BP; 319 A; 696 C; 659 G; 390 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                               Assay for alpha-2b adrenergic receptor ligands - using membranes of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hart1g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-2b adrenergic receptor; adrenoceptor; adrenaline; epinephrine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT59499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            produce antibodies for inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone NGC-alpha2beta was isolated from a human spleen genomic library screening with a fragment of the human 5-HTIA receptor gene. The gene be used to express recombinant receptor protein which can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 2; 15pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SYNA-) SYNAPTIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                   1997-107576/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transduction; neurotransmitter; ligand;
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  e alpha-2B
field.)
                                                                                                                                                                                                                                                                                                                                            recombinant
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91US-00707604
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91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RL
                       adrenergic
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                                                                                                                                                                                                                                                                                                                                          receptor.
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Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                     receptor. (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor function
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                       9
                       25-MAR-2003
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Sequence

2072 BP;

316

> 705

Ç 660 <u>ن</u>

391 T; 0 U; 0 Other

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cc polynucleotide probes comprising a sequence selected from one of the 1490 cc sequences mentioned in the specification. The combination is useful as an carray element in a microarray for monitoring the expression of a number cof diagnosis and treatment of cancer and immunopathology and neuropathology. Cc The microarray is useful in diagnostics and treatment regimens, drug cc discovery and development, toxicological and carcinogenicity studies, cc forensics and pharmacogenomics. The microarray is also useful for combination is also useful for purifying a subpopulation of mRNAs, cDNAs carray can detect changes in expression and diagnostic applications. The cc array can detect changes in expression in a large number of genes coding codifferent signaling pathway populations which can be used to diagnose covarious diseases including cancer e.g. adenocarcinoma and leukaemia, climmunopathies e.g. ALDs and asthma, neuropathes e.g. Alrheimer's disease cc and Parkinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence data for this patent did not cormat directly from USPO at the large counciled in electronic cormat convision user.
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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Combination of polynucleotide probes, useful as array elements microarray for monitoring the expression of a number of target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human signalling pathway polynucleotide probe SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a combination which, comprises a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1181; 65pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-352189/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-1998;
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                                seqdata.uspto.gov/sequence.html?DocID=06500938B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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91.7%;
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Pred. No. 0.02
0; Mismatches
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CC The present invention describes antigenic peptides (I) comprising: (a) CC any one of 1601 sequences (see ABP82019 to ABR83619) of 12-24 amino CC acids. Also described: (1) an assay for the detection of a particular GC and (2) an isolated antibody having high specificity and high affinity or CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an CC antibody against a particular GPCR. (I) can be used as GPCR modulators and in the production of specific CC antibodies. The peptides and antibodies are also useful for detecting an CC presence or absence of corresponding GPCRs. The antigenic peptides for CC GPCRs and antibodies are useful for detecting the CC treating immune-related diseases, growth-related diseases, cell groliferative or autoimmune diseases, growth-related diseases, cell groliferative of corresponding GPCRs. AlDS, Alzheimer's disease, CC atherosclerosis, bacterial, fungal, protozoan or viral infections, corresponding, allergies, Crohn's disease, diabetes, graft versus host corresponding and designing drugs for CC disease, parkinson's disease, multiple sclerosis, pain, psoriasis,
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                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 1; 523pp; English.
                                                                                                                                                                                                                                                                                                                                                                        New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein-coupled receptor; GPCR, antigenic peptide; gene therapy; growth-related disease; cell regeneration-related disease; ammunological-related cell proliferative disease; autoimmune disease; ALDS; cancer; altheoperosis; disease; atherosclerosis; infection; osteoparthritis; allergy; osteoporosis; cardiomyopathy; inflammation; Crohn's disease; disease; graft versus host disease; Parkinson's disease; multiple sclerosis; pain; mental retardation; epilepsy; asthma; tuberculosis; dementia; memory loss; hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIFE-) LIFESPAN BIOSCIENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-DEC-2001; 2001WO-US050107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roush CL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brown JP
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91.7%;
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Pred. No. 0.02
0; Mismatches
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RESULT 14
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                            tumour-associated antigen. The cDNA is useful in gene therapy and as an oligonucleotide probe for detecting mRNA coding for the melanome associated antigen in a sample. The cDNA is useful for vaccinating an individual who is at risk of getting cancer, suspected of having cancer cor has cancer. The present sequence is useful for vaccinating an melanoma tumour by inducing an immune response against it. The melanoma of melanoma, monitoring metastatic melanoma, as new targets for recurrence and metastatic disease to be detected and disease burden of particular use in melanom of the melanoma tumour-associated antigen is melanoma to be detected and disease burden.
       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 44
                                                                                                                                                                      The present sequence is 3' end cDNA
                                                                                                                                                                                                               Claim 1; Fig 2G; 55pp; English.
                                                                                                                                                                                                                          Isolated DNA sequence encoding a melanoma tumor associated antigen, useful for detection, diagnosis and staging of melanomas, monitoring metastatic melanomas and as a target for immunotherapy.
                                                                                                                                                                                                                                                                                                   WPI; 2001-308473/32.
                                                                                                                                                                                                                                                                                                                                                      (UABR-) UAB RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2000; 2000WO-US041260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; melanoma tumour-associated antigen; cytostatic; gene therapy; vaccine; cancer; immune response; metastatic melanoma; immunotherapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3' end of human melanoma tumour-associated antigen cDNA from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anxiety, depression, schizophrenia, dementia, mental retardation, memo 1088, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode GPCR proteins given in ABP81675 to ABR82018, which are used in the exemplification of the present invention
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44; Conservative
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                      use in melanoma research
                                                                                                                                                                                                                                                                                                                             Conry RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
158 A; 115
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91.7%;
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Pred. No. 0.02:
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                                                                                                                                                                        human melanoma
                          antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone 5.31.
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Query Match Best Local Similarity

Matches

42;

Conservative

0,

71.8%; 82.4%;

Score 36.6; Pred. No. 0.

DB 4; Τ, 0 U;

Length 593;

9;

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Gaps

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G; 174

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GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGTGTGAACCCCAG

51

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The invention relates to novel purified or isolated nucleic acids of CC essential genes of Aspergillus funigatus. The isolated nucleic acids of the invention are used to treat or prevent infections by a pathogenic cC organism such as A. funigatus, to treat a non-infectious disease in a subject (e.g. cancer), to prevent or contain contamination of an object cby A. funigatus, or to prevent or inhibit formation on a surface of a cC biofilm comprising A. funigatus. The polynucleotides are useful for cx therapeutic use, as markers for host tissues in which the pathogenic cryanisms invade or reside, for comparing with the DNA sequence of A. CC funigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and cc making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anni-protein antibodies, as an capture to raise anti-DNA antibodies or to elicit another immune constitution. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for constitution of the pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence cf factors. This polynucleotide sequence represents one of the essential cc genes of Aspergillus funigatus of the invention
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27-APR-2001; 2001US-0287066P.
05-JUN-2001; 2001US-0295890P.
09-JUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page; 175pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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Sequence 2367 BP; 630 A; 644 C;

681 G;

412 T; 0 U; 0 Other;

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CC subject (e.g. cancer), to prevent or contain contamination of an object (c) yA, funigatus, or to prevent or inhibit formation on a surface of a color biofilm comprising A, funigatus. The polynucleotides are useful for chiefly comparising recombinant protein for characterisation, screening or corpanisms invade or reside, for comparing with the DNA sequence of A. CC funigatus to identify duplicated genes or paralogues having the same or comparisms invade or reside, for comparing with the DNA sequence of A. CC funigatus to identify duplicated genes or paralogues having the same or comparisms invade or related or distant pathogenic organisms to identify sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and comparing objecting antibodies or to elicit another immune comparing objections encoding the other protein comparing objections objections encoding the other protei
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05-JUN-2001; 2001US-0295890P
09-JUL-2001; 2001US-0303899P
31-AUG-2001; 2001US-0316362P
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cancer; contamination;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New purified or isolated nucleic acids of essential genes of Aspergillus
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The invention relates to novel purified or isolated nucleic acids of CC essential genes of Aspergillus funigatus. The isolated nucleic acids of CC the invention are used to treat or prevent infections by a pathogenic CC organism such as A. fumigatus, to treat a non-infectious disease in a CC subject (e.g. cancer), to prevent or contain contamination of an object CC subject (e.g. cancer), to prevent or inhibit formation on a surface of a CC by A. fumigatus, or to prevent or inhibit formation on a surface of a CC proposition of a contain contamination of an object CC proposition of the protein for contain contamination of an object CC proposition of the pathogenic CC contains invade or reside, for comparing which the pathogenic CC configatus to identify duplicated genes or paralogues having the same or configatus to identify duplicated genes or paralogues having the same or sequences of other related or distant pathogenic organisms invade or related or distant pathogenic organisms to identify contential orthologous essential or virulence genes, for selecting and contential orthologous essential or virulence genes, for selecting and contained to relate the pathogenic organisms to identify contained to relate and for identifying polynucleotides or to elicit another immune contained to relate the protein antibodies, as an interaction. The polypeptides may be used to raise antibodies or to identify the binding coccurs or to identify inhibitors of the binding coccurs or to identify inhibit
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                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page; 175pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                             New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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27-APR-2001; 2001US-0287066P.
05-UUN-2001; 2001US-0295899P.
09-UUL-2001; 2001US-0303899P.
31-AUG-2001; 2001US-0316362P.
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CC The invention relates to novel purified or isolated nucleic acids of CC essential genes of Aspergillus fumigatus. The isolated nucleic acids of CC the invention are used to treat or prevent infections by a pathogenic CC organism such as A. fumigatus, to treat a non-infectious disease in a CC by A. fumigatus, to treat a non-infectious disease in a CC by A. fumigatus, to treat or contain contamination of an object CC confirm comprising A. fumigatus. The polynucleotides are useful for CC expressing recombinant protein for characterisation, screening or CC conganisms invade or reside, for comparing with the pathogenic CC fumigatus to identify duplicated genes or paralogues having the same or CC similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic cromparing with the DNA sequence of A. CC sequences of other related or distant pathogenic organisms to identify contential orthologous essential or virulence genes, for selecting and CC making oligomers for attachment to a nucleic acid array for examination confirm contention, as an
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                                                                                                                                                                                                                                                                                                               New purified or isolated nucleic acids of essential genes of Aspergillus fumigatus, useful for treating or preventing infections by A. fumigatus, or for treating a non-infectious disease in a subject e.g. cancer.
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27-APR-2001; 2001US-0287066P.
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09-UUL-2001; 2001US-0303899P.
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cancer; contamination; biofilm; antibody; immune response; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polynucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELITRA PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Tishkoff D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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88.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>,</u>
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Pred. No. 0.89
0; Mismatches
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RESULT 19
AACS4146 6
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AACS4146 6
XX
ACS4146;
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ACCS4146;
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ACCS414
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Best Local S
Matches 39
  25-FEB-1999

05-MAR-1999

23-MAR-1999

25-MAR-1999

25-MAR-1999

26-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-APR-1999

25-MAY-1999

06-MAY-1999

06-MAY-1999

11-MAY-1999

11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case or virulence factors. This polynucleotide sequence represents one of the essential genes of Aspergillus fumigatus of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene eprotein identification; signal transduction
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39; Conserv
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  99US-0121825P

99US-0123180P

99US-0125788P

99US-0126785P

99US-0126785P

99US-0126785P

99US-0126785P

99US-0130677P

99US-0130677P

99US-0130610P

99US-0131449P

99US-0132485P

99US-0132485P

99US-0132485P

99US-0132485P

99US-0132485P

99US-0132485P

99US-0134256P

99US-013421P

99US-013421P

99US-013421P

99US-013421P

99US-0134376P

99US-0134376P
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0.9;
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      08-JUN-1999
110-JUN-1999
110-JU
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21-MAY-1999
24-MAY-1999
25-MAY-1999
27-MAY-1999
28-MAY-1999
01-JUN-1999
03-JUN-1999
04-JUN-1999
04-JUN-1999
99US-0135124P

99US-013553P

99US-013562P

99US-0136782P

99US-0137752P

99US-0137782P

99US-013847P

99US-0138487P

99US-0138487P

99US-0138487P

99US-0138487P

99US-0138482P

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99US-0138482P

99US-0138482P

99US-0138482P

99US-014882P

99US-013884P

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02-AUG-1999, 02-AUG-1999, 02-AUG-1999, 02-AUG-1999, 03-AUG-1999, 04-AUG-1999, 04-AUG-1999, 05-AUG-1999, 05-AUG-1999, 06-AUG-1999,

99US-0146386P 99US-0146388P 99US-0147038P 99US-0147038P 99US-0147302P 99US-0147302P 99US-0147302P 99US-0147303P 99US-0147303P

09-AUG-1999; 09-AUG-1999; 10-AUG-1999;

99US-01474935 99US-0149355 99US-01481715 99US-0148315 99US-01483415 99US-01483415 99US-01485655

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                               Query Match
Best Local Similarity
Matches 38; Conserve
                                                                                        RESULT 20
AAQ88817
ID AAQ88
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                                                                                   Porcine and human SPAR cDNAs were compared. They are highly homologous, divergent. The 32.3 kDa human and 3.8 kDa porcine ORFs are sinular. Both The projected secondary structure of highly nor is similar. Both porcine counterpart. The pSPAR protein is predicted to have a hydrophoic a second alpha helix of 28 residues beginning at AA 48. It is followed by a turn, pleated sheets. Human SPAR ORF has a 25 AA hydrophobic and treesidue 29, followed by beta-pleated sheets and turns. Another 28 residue beta- helix begins near AA 200. (Updated on 25-MAR-2003 to correct pN field.)
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PR
PR
PR
                                                                            Sequence 1820 BP; 501 A; 393
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Best Local S
Matches 38
                                                                                                                                                                                                                                                      Compsn. capable of binding to surfactant protein-A receptor - which modulates secretion of alveolar surfactant, e.g. to treat respiratory
                                                                                                                                                                                                                                Disclosure; Page 35-36; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                         31-AUG-1993;
30-DEC-1993;
                                                                                                                                                                                                                                                                                                    WPI; 1995-115402/15.
P-PSDB; AAR71460.
                                                                                                                                                                                                                                                                                                                                  Strayer DS,
                                                                                                                                                                                                                                                                                                                                                 (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-1994;
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09-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPAR; surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human surfactant protein A receptor (hSPAR) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTG
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                                     milarity 88.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L Similarity 88.4
38; Conservative
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(first entry)
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93US-00176218.
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99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
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88.4%;
                                 ; Score 35; DB 2
; Pred. No. 1.6;
0; Mismatches
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                                                                         C; 418 G; 508 T;
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                                5; Indels
                                                                       0 U; 0 Other;
                                                 Length 1820;
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10-SEP-1999; 13-SEP-1999; 15-SEP-1999; 16-SEP-1999; 20-SEP-1999;

18-AUG-1999 20-AUG-1999 20-AUG-1999 20-AUG-1999 23-AUG-1999 23-AUG-1999 23-AUG-1999 26-AUG-1999 27-AUG-1999 27-AUG-1999

22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 28-SEP-1999; 29-SEP-1999;

99US-0148648 99US-0149368 99US-0149126 99US-0149722 99US-0149929 99US-0149929 99US-0150866 99US-0151066 99US-0151066 99US-0151066 99US-0151069 99US-0151069 99US-0151069 99US-0151069 99US-0151069 99US-0151069 99US-0154018 99US-0154018 99US-0154018 99US-0154018 99US-0154018 99US-0154018 99US-0154018 99US-0154018 99US-0154018 99US-015545 99US-015545 99US-015545 99US-015545 99US-01565 99US-01565 99US-015939 99US-0160767 99US-0160981 99US-0160981 99US-0160981 99US-0161406 99US-0161406 99US-0161406 99US-0161406 99US-0161406 99US-0161406 99US-0161406 99US-0161406

04-OCT-1999 05-OCT-1999 06-OCT-1999 07-OCT-1999 08-OCT-1999 12-OCT-1999 13-OCT-1999 13-OCT-1999

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572

GAAGATGATGAAGAGGAGGAGGAAGAAGAAGAATGTG

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Sequences ABP31028-ABP35561 represent 4534 novel human proteins
CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC ABN79587 represent cDNAs encoding them. The invention also encompasses
CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
CC polynucleotides, the recombinant production of ORFX proteins, antibodies
CC polynucleotides, methods of detecting ORFX proteins, antibodies
CC polynucleotides, methods of screening for modulators of ORFX expression or
CC cartivity, and methods of screening individuals for a predisposition to an
CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
CC range of biological activities, such as cytokine, cell proliferation,
CC cissue growth, angiogenesis, activin or inhibit activity, chemotactic/
CC chemokinetic activity, haemostatic activity, thrombolytic activity,
CC and antiinfective activity, and may also be involved in the determination
CC of bodily characteristics, fertility and behaviour. ORFX proteins,
CC other proliferative disorders such as epilepsy and Alzhatment of cancers,
CC cardiovascular diseases, immune system disorders, disorders related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 1036; 2508pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis replation; thesue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-106200/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-2000; 2000US-0206690P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-2001; 2001WO-US017076.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperproliferative disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200190366-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABN76609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN76609 standard; cDNA; 392 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shimketa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:3111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         related to organ
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RESULT 22
ANV25477
ID ANV25
XX AV25
XX AV25
XX AV25
XX POCAS
XX POCAS
XX RAt s
XX POCAS
XX New
PT Crea
XX Clai
XX Clai
XX Clai
XX Sequ
SQ Sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases
 Sequence 5000 BP; 1238 A; 1287 C; 1243 G;
                                                            The present sequence encodes a new sulphonylurea receptor (SUR2) isolated from a rat brain cDNA library. The sequence can be derivantials such as human or rat. Products of SUR2 can be used for di
                                                                                                                                                      New sulphonyl-urea receptor protein - useful treatment of potassium channel diseases such
                                                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAV25477 standard; cDNA; 5000
                                                                                                                            Claim
                                                                                                                                                                                                                      WPI; 1998-200632/18.
                                                                                                                                                                                                                                                     (NICH-)
                                                                                                                                                                                                                                                                                                  09-AUG-1996;
                                                                                                                                                                                                                                                                                                                                 09-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                               JP10052275-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     potassium channel disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; sulphonylurea receptor; SUR2; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat sulphonylurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV25477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 392
                                               treatment of potassium
                                                                                                                           2; Fig 7-11; 19pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85
                                                                                                                                                                                                                                                   KIYONO
JAPAN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGA 44
                                                                                                                                                                                                       AAW53602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGATGAGGAAGAAGAGGAGGAGGAAGAAGAGGGAAGA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 116 A; 64 C; 112 G; 100 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                   CHEM RES
                                                                                                                                                                                                                                                                                                96JP-00227552
                                                                                                                                                                                                                                                                                                                               96JP-00227552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
271. .4908
                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "SUR2"
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "sulphonylurea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor SUR2 encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.5%;
                                                                                                                                                                                                                                                     8
                                                                                                                         Japanese.
                                               channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
                                               diseases, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB
 1232 T; 0 U; 0 Other
                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
                                                                                                                                                                        for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6,
                                                                                                                                                          ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 392;
                                               hypertension
                                                                                                                                                                        e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                       diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholesterol ester
l, bacterial,
                                                                            r (SURZ) protein
be derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Query Match

67.5%;

Score 34.4;

DB

<u>ب</u>

Length 5000;

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ABSULT 23
ABT4189
ID ABT4189
ID TOXIC
XX ABT411
AC ABT41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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The invention relates to a novel method of predicting at least one toxic effect of a compound. The method comprises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the progression of a toxic effect of a compound, predicting the toxicity of a compound, or identifying toxicity markers in tissues or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAY-2001; 2001US-0292335P.
13-UUN-2001; 2001US-029925P.
10-UUL-2001; 2001US-029925P.
10-UUL-2001; 2001US-030380PP.
10-UUL-2001; 2001US-030380PP.
10-UUL-2001; 2001US-0315047P.
28-AUG-2001; 2001US-0315047P.
27-SEP-2001; 2001US-0324928P.
27-OCT-2001; 2001US-0330867P.
21-NOV-2001; 2001US-0330867P.
21-NOV-2001; 2001US-0331805P.
21-NOV-2001; 2001US-0331805P.
21-PEB-2002; 2002US-0357844P.
19-DEC-2001; 2001US-0357844P.
21-PEB-2002; 2002US-0357844P.
21-PEB-2002; 2002US-0357844P.
21-PEB-2002; 2002US-0357844P.
21-PEB-2002; 2002US-0357844P.
08-APR-2002; 2002US-037044P.
08-APR-2002; 2002US-0370206P.
08-APR-2002; 2002US-0370206P.
08-APR-2002; 2002US-0370206P.
08-APR-2002; 2002US-0370206P.
08-APR-2002; 2002US-0370206P.
08-APR-2002; 2002US-0370206P.
08-APR-2002; 2002US-0370204P.
21-APR-2002; 2002US-037024P.
                                                                                                                                                                                                                                                                                                                                                                          Predicting
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-148464/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mendrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200295000-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxicity modelling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        database;
                                                                                                                                                                                                                                                                                        teast l sample exposed t sile to a data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABT41889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3109 GAGGATGAAGATGAAGAGGAGGAGGAGGAAGATGAGGACGA 3152
                                                                                                                                                                                                                                        4; Page; 446pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           effect; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   μ
                                                                                                                                                                                                                                                                                                                                                                        at least
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAAGTGTGA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porter M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOGIC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002US-0371679P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002WO-US016173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening;
                                                                                                                                                                                                                                                                                        one toxic effect of a compound, useful for toxicity preparing a gene expression profile of a tissue or to the compound, and comparing the gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression profile; renal toxicity; toxicity marker; eening; toxicity assay; rat; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ζ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Higgs B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID No 1591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elashoff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Σ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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RESULT 24
ADBS8175
ADBS8175
AND BS8175
AXX ADBS8
AXX ADBS8
AXX ADBS8
AXX Toxic
AXX IN-I,
AXA IN-
CC The present invention relates to a method for predicting a toxic effect CC of a tompound. The method comprises preparing a gene expression profile CC of a tissue or cell sample exposed to the compound, and comparing the CC differential expression of the compound, and comparing the CC differential expression of the gene indicates at least one toxic effect. CC compound, predicting appearance to the strong confidence of a compound, identifying an agent that modulates the onset or compound, identifying an agent that modulates the onset or CC progression of a toxic response, predicting the cellular pathways that a CC compound modulates in a cell, and identifying an agent that modulates at CC least one activity of a protein. The method and compositions of the progression, are useful in identifying toxicity markers in a cell situations of the confidence of the confide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 3201; 1156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprises preparing gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Predicting a toxic effect markers in liver tissues o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-2002; 2002US-00060087.
15-MAR-2002; 2002US-0364045p.
15-MAR-2002; 2002US-0364055p.
30-DEC-2002; 2002US-0436643p.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mendrick D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-2003; 2003WO-US003194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toxicity-related gene, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Toxic; toxin; gene expression profile; hepatotoxicity; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADB58175;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease physiological states, or disease progression. This polynucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this pate did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5000 BP; 1238 A; 1284 C; 1246 G;
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86.4%;
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Pred. No. 2.4;
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RESULT 25
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08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-MAY-2002;
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13-MAR-2002;
08-APR-2002;
                                                                                                                                   Mendrick
Elashoff
The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to
                                                                     Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene express profile of a tissue or cell sample to a database of Tox mean and non-
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11-APR-2002;
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2002US-0378370P.
2002US-0378652P.
2002US-0378653P.
2002US-0378665P.
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RESULT 26
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                                                                                                                               Purified nucleic acid encoding Insulin Receptor Substrate - us prepare IRS-1, for diagnosis and treatment of insulin related and abnormal cellular proliferation.
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17-MAR-1993
                                                                                                         Disclosure; Fig
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                                                                                                        128pp; English.
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The sequence given encodes the rat insulin receptor substrate-1 (IRS-1). The IRS-1 was isolated using the probe sequences given in AAQ29701-02. The IRS-1 sequence can be inserted a vector and used to transform cells to produce IRS-1. The level of IRS-1 metabolism can then be studied and abnormal levels may be seen to be indicative of insulin related disease. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 5125

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sequences. (I) is useful as hybridisation probes, polymerase chain (CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used (CC and in recombinant production of (II). The polymucleotides are also used (CC genes. (I) is useful in gene therapy techniques to restore mapping, (CC genes. (I) is useful in gene therapy techniques to restore mormal (CC useful for generating antibodies against it, detecting or quantitating a (CC useful for generating antibodies against it, detecting or quantitating a (CC useful for generating antibodies against it, detecting or quantitating a (CC involving aberrant protein expression or biological for treating disorders (CC usephenetics, forensics, gene mapping, identification of mutations (CC diagnostics, forensics, gene mapping, identification of mutations (CC and to produce other types of data and products dependent on DNA and (CC coding sequences AAS64197-AAS94564 represent novel human diagnostic (CC antion of the present in the printed specification, but was obtained in (CC electronic format directly from WIPD)
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                                                                                                                                                                                                                                                                                                                                      The invention
                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 4730; 103pp; English
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23-AUG-2000; 2000US-00649167,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #4730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food supplement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS68926 standard; cDNA; 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001-639362/73.
DB; ABG04739.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome mapping; gene mapping; gene therapy; forensic;
upplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
            B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GĠĀĠĠĀĠĠĊĀĠĀĠĠĀĠĠĀĠĠĀĠĠĀĠĀĀĠĠĀĠĠĀĠĠĀĠĠĀĠĀĠĀĀĊĊĊĊ
                                                                                                                                                                                                                                                                                                 relates to isolated polynucleotide (I) and polypeptide (II) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
129 A; 22 C; 112 G; 28 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tang
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83.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34.2; DE Pred. No. 2.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ν.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
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Best Local Similarity

66.3%; 84.4%;

Score 33.8; Pred. No. 3;

DΒ 5 Ģ,

Sequence 1018 BP; 333 A;

243 Ç

265

G;

177 ; 0 Ģ

0 Other;

0 Other,

Query Match

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ABZ24593
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                                                                                                                     Disclosure; Page 111-112; 141pp; English.
                                                                                                                            New ovary-specific-genes comprising O1-180 or O1-236, useful for decreasing conception or enhancing fertility, or for the preparation composition for treating e.g. cancer.
                                                                                                                                                       P-PSDB; ABP58237
                                                                                                                                                                    Matzuk MM, Wang P,
                                                                                                                                                                                            27-APR-2001; 2001US-00844864.
                                                                                                                                                                                                     26-APR-2002; 2002WO-US013245.
                                                                                                                                                                              (BAYU) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                Ovary; O1-236; mouse; nucleoplasmin 2; Npm2; contraceptive; antiinfertility; cytostatic; gene therapy; gene; ss.
                                                                                                                                                                                                                           WO200288314-A2
                                                                                                                                                                                                                                                             Mus musculus.
                                                                                                                                                                                                                                                                                    Mouse ovary-specific 01-236 cDNA.
                                                                                                                                                                                                                                                                                                31-MAR-2003
                                                                                                                                                                                                                                                                                                          ABZ24593;
                                                                                                                                                                                                                                                                                                                 ABZ24593 standard; cDNA; 1018
                                                                                                                                                           2003-167110/16.
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                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                               (first
                                                                                                                                                                                                                                 /product= "Murine O1-236"
                                                                                                                                                                                                                                              156. .779
                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                              entry)
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DB

Length 1018;

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RESULT 29
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ID AADD00
XX AAD
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Best Local S
Matches 38
                                                                           The present sequence is the mouse oocyte-specific gene Npm2, complete cDNA clone 01-236. It is derived from mouse 2-cell embryo cDNA library and expressed in the oocytes of intermediate size type 3a follicles and all type 3b follicles. This clone is used to screen and identify the mouse Npm2 gene. It is homologous to Xenopus laevis nucleoplasmin (Xnpm2) expressed exclusively in eggs. It provides in vitro and in vivo reagents for studying ovarian development and function. This sequence has gynaecological and contraceptive activity. Agents which modulate 01-180, 01-184 and 01-236 may be used to treat cell proliferative or degenerative genes. This ovary-specific sequence can be used as reagents to evaluate potential contraceptives, to block ovulation in a reversible manner. It is also used to screen for genetic mutations in signalling pathways, that are associated with some forms of human infertility or gynaecological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01\text{-}180, 01\text{-}184 and 01\text{-}236 polypeptides and nucleic acids encoding useful for evaluating potential contraceptives to block ovulation reversible manner.
  Sequence 1019 BP; 334 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oocyte-specific; ovary; O1-236; mouse; Npm2; gynaecological; treatment; nucleoplasmin; cell proliferative disorder; cell degenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 22; Fig 5; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matzuk MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200024755-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ecreen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse oocyte-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD00296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ovulation; signalling pathway; human infertility; cancer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0106020P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US025209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "Mouse oocyte-specific protein, 01-236"
/note= "Identical to mouse Npm2 protein with the
exception of one residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O1-236 cDNA clone
  243
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВÞ
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  265
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  U; 0 Other
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                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                       Occyte-specific; ovary; Npm2; nucleoplasmin; mouse; mammalian ortholog; chromosome 14; human chromosome 19; contraceptive; gynaecology; cance: cell proliferative disorder; cell degenerative disorder; ovulation; modulator; human infertility; signalling pathway; screen; treatment; ds
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                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse ovary-specific Npm2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-SEP-2000
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                                                                                                                                                                                                                             intron
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
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                                                                                                   /*tag= j
/note= "The /
512..542
/*tag= k
/number=
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527
                                                                                                                                                                                                          395. .425
/*tag= g
/number= 2
                         /number= 4
657. .687
                                                 between bases
543. .656
                                                        /*tag= 1
/note= "Corresponds
/note= bases 526 an
                                                                                                                                              /*tag= i
/number= 3
                                                                                                                                                               2 between 426. .511
                                                                                                                                                                                                   410
                                                                                                                                                                                                                                                                                                                                          200. .230
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
151. .199
                                                                                                                                        473
                                                                                                                                                                  /*tag= h
/note= "Corresponds to 105 missing nucleotides of intron
2 between bases 409 and 411"
                                                                                                                                                                                                                                              /*tag= f
/product=
                                                                                                                                                                                                                                                              /number= 2
337. .1177
                                                                                                                                                                                                                                                                                                                                                           /*tag= b
/number= 1
                                                                                                                                                                                                                                                                                               /*tag= d
/note= "Corresponds to 314 missing nucleotides of intron
1 between bases 214 and 216"
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                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                       231. .394
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                        .687
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                                                                                                                                                                                                                                     "Coding
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                                                                                                                                                                                                                                    "Mouse ovary-specific Npm2 protein" oding region is interrupted by 8 introns"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33.8; DI
Pred. No. 3.2;
0; Mismatches
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01-180, 01-184 and 01-236 polypeptides and nucleic acids encoding useful for evaluating potential contraceptives to block ovulation reversible manner.
                                                                                            WPI; 2000-350684/30.
P-PSDB; AAY70951.
                                                                                                                                                Matzuk MM, Wang P;
                                                                                                                                                                                                                                     28-OCT-1998;
                                                                                                                                                                                     (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                         28-OCT-1999;
                                                                                                                                                                                                                                                                                                                  04-MAY-2000.
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/note= "Corresponds to 471 missing nucleotides of intron
7 between bases 1051 and 1053"
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/note= "Corresponds to 1321 (1.32kb) missing nucleotides
of intron 5 between bases 796 and 798"
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/note= "Corresponds to 2771 (2.77kb) missing nucleotides
of intron 4 between bases 671 and 673"
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Search completed: February 29, 2004, 20:36:16
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Matches 38
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                                             Score
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1 gaggatgaagctgaagagga.....aggaagagtgtgaaccccag
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1044)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                             Homo sapiens
                                                                                                                        Homo sapiens (human)
                                                                                                                                              BQ880026.1 GI:22272034
                                                                                                                                                               BQ880026 1044 bp mRNA linear EST 16-AUG-2002
AGENCOURT 8113358 Lupski_dorsal_root_ganglion Homo sapiens cDNA
Clone IMAGE:6179035 5', mRNA sequence.
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Similarity 91.7%;
44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Adams,M.D. and Cargill,M.

Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 135)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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Science 302 (5652), 1960-1963 (2003)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens HCM6030 gene,
genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1. >1353
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                                                                                                                                                                                                                                                                                          Score 41.6; DE Pred. No. 11; 0; Mismatches
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1e, VIRTUAL TRANSCRIPT, partial sequence,
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Gene Collection (MGC)

Euteleostomi; Homo.

Indels Length 1353;

Gaps

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                                                                                                   Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Direct Submission
                                                                                                                                                                                                                                                                                         1 (bases 1 to 1347)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                           Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                            (bases 1 to 1347)
                                       sequence was made by sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop: 430.
                 based on alignment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Lupski_dorsal_root_ganglion"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
/note="Yector: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACCGGTCCG-3' and
5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
|mol_type="mRNA"
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98.1%;
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ne, VIRTUAL
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23;
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                                       genomic
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                                                                                  45 West Gude Drive,
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Matches
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                                                                                                                                                                                                AL872808
AL872808 )
                       1 (bases 1 to 633)
Croning,M.D.R., Ashurst,J.L.,
Sanger Xenopus tropicalis EST
Unpublished (2003)
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                                                                                                                    Silurana tropicalis (western clawed frog) Silurana tropicalis
                                                                                                                                                                                                                                                                                                                                   43,
On Sep 15, 2002 this sequence version replaced gi:22893073 Contact: Taylor R
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                        sequence.
AL872808
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Hunter, C. and Elgar, G.
Alpha2 adrenergic receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS; Alpha2 adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL606560
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                                                                                                                                                            AL872808.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biohelp@hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Centre Hinxton, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (14-SEP-2001) MRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hunter, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Equus caballus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Equus caballus (horse)
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                                                                              Kenopodinae; Silurana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 872)
                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                 XGC-egg Silurana
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Equus caballus"
/mol_type="genomic DNA"
/db_xref="taxon:9796"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                            GI:38666205
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86.0%;
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Pred. No. 55;
0; Mismatches
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Pred. No. 43;
O; Mismatches
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                                      Taylor, R., Zorn, A.M. a project 2001 (11_2003)
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TEgg106k18 5', mRNA
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                                                    and Rogers, J
                                                                                           Euteleostomi; 
; Pipidae;
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RESULT 6
AL852740/c
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                                                                        Sanger Institute

Sanger Institute

Hinxton, Cambridgeshire, CB10 1SA, UK

Email: trop@sanger.ac.uk

Sanger Xenopus tropicalis EST project 2001

TROPICALIS SEQUENCE ID: TEgg015d14.plkSP6

Sequencing primer: SP6

Constructed by Aaron M. Zorn.

CDNA was oligo dT primed from Sug of poly A+ RNA from egg.

S' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI

Host: Escherichia coli XL1-blue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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                                                                                                                                                                                                                                                                                                                                          Croning M.D.R., Ashurst, J.L., Taylor, R., Zorn, A.M. and Roge Sanger Xenopus tropicalis EST project 2001 (11_2003) Unpublished (2003) On Sep 15, 2002 this sequence version replaced gi:22872961 Contact: Taylor R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Silurana tropicalis (western clawed frog) Silurana tropicalis
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AL852740 XGC-egg Silurana tropicalis
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Sequencing primer: $\frac{7}{8}6$
This sequence is from a Xenopus Gene Collection (XGC) library constructed by Aaron M. Zorn.

CONA was oligo dT primed from Sug of poly A+ RNA from egg. EcoRI-Not1 cut cDNA was then ligated into pCS107 with EcoRI at yend and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site_2: NotI

Host: Escherichia coli XLI-blue.
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                     /organism="Silurana tropicalis"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clome_lib="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"
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85.7%;
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_xref="taxon:8364"
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Pred. No. 64;
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RESULT 8
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ORIGIN

FEATURES

REFERENCE AUTHORS

TITLE

SOURCE VERSION KEYWORDS ACCESSION

ORGANISM

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KEYWORDS
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                      1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204
                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                             Plate: SRG8014 row: O column: 4 Seq primer: TAGAAGGCACAGTCGAGG.
                                                                                                                                                                                                                                                                                                                                                                                    Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: SRG8014 row: O column: 4
GAĞĞAĞĞAAĞATĞAAĞAĞĞAĞĞAAĞAĞĞAAĞAAĞAĞAĞTĞAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 642)
Smith, T. P. L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.

A second set of porcine ESTs from a pooled-tissue normalized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF360731 642 bp mRNA linear CF360731 642 bp, mRNA linear CF360731
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                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.1%; Score 37.8; ilarity 85.7%; Pred. No. 64; Conservative 0; Mismatches
                                                                                                                                                                                                                                                 /organism="Sus scrofa"
/mol_type="mxNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DHIOB"
                                                                                                                                                      /clone lib="MARC 3PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
/ibrary made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."
                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="XGC-egg"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cI was oligo dr primed from 5ug of poly A+ RNA from egg. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:8364"
/clone="TEgg015d14"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
                                                                                           72.5%;
88.9%;
                                                                        Score 37; DB:
Pred. No. 96;
0; Mismatches
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•
                                                                                                      Length 642;
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AUTHORS
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AUTHORS
TITLE
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DEFINITION
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ORGANISM
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Best Local Similarity
    TITLE
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                                                                                                                                                                                                                                                                                                                                                                                            41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
                                                                                                                Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                       BZ195097
CH230-248P14.TV CHORI-230 Segment 2 Rattus CH230-248P14, genomic survey sequence.
Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Riggs,P., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tags from Canine heart Unpublished (2003) Other ESTs: CH3#019 B01T3
                                                                                                                                                                                                                 BZ195097
BZ195097.1 GI:23853149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: al.george@vanderbilt.edu
Insert Length: 1072 Std Error:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 615 936 2660
Fax: 615 936 2661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vanderbilt University
529 Light Hall, 2215 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU748295
BU748295.1 GI:23700479
EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BU748295 787 bp mRNA linear EST 10-OCT-20 CH3#019_B01T7 Canine heart normalized cDNA Library in pBluescript Canis familiaris cDNA clone CH3#019_B01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Division of Genetic Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: George AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canie familiarie
                                                                                                  Kaccus
                                                                                                                                                                          Rattus norvegicus (Norway rat)
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                                                                                                                                                                                                                                                                                                                                                                                            GATGAAGAAGCAGAAGAGGAGGAGGAGGAGGAAGAGAGGATGAA 85
                                                                            (bases 1 to 770)
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Y., Desai,R., Ol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: heart; Vector: pBluescript; Site_1: 5' of vector NotI; Site_2: 3' of vector EcoRI; Fissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, poincer, Irish setter). Library construction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligo-dT primed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pBluescript"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="heart"
/cell_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Canis familiaris"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="Canine heart normalized cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dev_stage="mixed developmental stages (adult, 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="CH3#019_B01"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olarte, M., Henthorn, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; Pred. No.
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  Library CHORI-230 MboI segment
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99;
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                                    Geer,K.,
Russell,D.,
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                                                                                                                                                                                                                                                                                           GSS 11-OCT-2002
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Canis.
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                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAAC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 256)
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page: http://www.tigr.org/tdb/bac_endB/rat/bac_end_intro.html
plate: 248 row: P column: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Other_GSSs: CH230-248P14.TJ
Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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Fax: 301 838 0208
                                                                       sequence:
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                                                                           The following repetitive elements were found in this cDNA requence: 37-156, >(GGA)n#Simple_repeat (matched complimen
                                                                                                                                                                                          This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
e: 37-156, >(GGA)n#Simple_repeat (matched co
>(GAA)n#Simple_repeat (matched compliment)
#Simple_repeat (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell type="Brain"
/clone_lib="CHORI-230 Segment 2"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: Mb
/note="Vector: pTARBAC1.3; Site_2: Mb
/note="Vector: pTARBAC1.3; Site_2: Mb
/note="Vector: pTARBAC1.3; Site_2: Mb
/note="Vector: pTARBAC1.3; Site_2: Mb
/note="Textor: pTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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/clone="CH230-248P14"
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/strain="BN/SsNHsd/MCW"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:24533352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             row: P
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87.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
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No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BMAP
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FEATURES source

Seq

primer: pyx-5

/mol\_type="mRNA" /strain="C57BL/6" 'organism≃"Mus musculus" ocation/Qualifiers

xref="taxon:10090"

/mol\_type="mRNA" /db\_xref="taxon:10090" /clone="IMAGE:1295340" organism="Mus musculus"

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Fax: 314 200 1011
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ;
info@image.llnl.gov) for further j
                                                                                                                                                                     Contact: Marra M/Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Lc Fax: 314 286 1810
                                                                                 Seq primer: -28ml3 revl ET from Amersham
High quality sequence ston. 340
                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 490); National, Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Waterston, R., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Materston, R.
                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                    Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA896321 490 bp mRNA linear EST 06-APR-1990 clone IMAGE:1295340 5, similar to gb:X56135 Mouse mRNA for AA896321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA896321.1 GI:3032714
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//dev stage="mbbyo 13 5,14.5,16.5,17.5dpc"
//lab host="phioB (TI phage resistant)"
//clone_lib="NIH_BMAP_FWO"
//clone_lib="NIH_BMAP_FWO"
//note="Organ: Brain, Vector: pXY- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
196. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
size selected according to mRNA size fraction, ligated
directionally into pXX-Asc vector. The library tag
is AGCGAGAGA. This library was created for the University
Developing Mouse Nervous System", supported by National
Program coordinator. "
                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="whole brain"
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83.7%;
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Pred. No. 1.3e
0; Mismatches
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8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                  MO 63108
                                                                                                           information.
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     Query Match
Best Local Similarity
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VERSION
KEYWORDS
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AUTHORS
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ORGANISM
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CB625989
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                                                                                                                                                                                                                                                                       Seq primer: gta aaa cga cgg cca gtg.
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BACKWARD: gga aac agc tat gac cat
Plate: 15 row: O column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                       Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O.
85721-0088, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                        Email: http://genome.arizona.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jantasuriyarat, C., Lu,G., Gowda,M., Hatfield,J., Zhou Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. Large-scale identification of ESTs involved in the in Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Rod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB625989
763 bp mRNA linear EST 08 clone OSIIEa15013.f OSIIEa Oryza sativa (indica cultivar-group) CB625989
CB625989.1 GI:29620978
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                                                                /clone="OSITEALSO13"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSITEA"
/note="Vector: pBluescript I.
XhoI; Lesion Mimic SPL 11"
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                                                                                                                                                                                           /organism="Oryza sativa (indica cultivar-group)"
|mol_type="mRNA"
|cultivar="IR36"
                                                                                                                                                                                     db_xref="taxon:39946"
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88.6%;
 Score 36;
Pred. No.
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Micmatches 5;
; DB 14;
. 1.6e+02;
                                                                               II KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   involved in the interaction
                                                                                                                                                                                                                                                                                                                                                                                                                               Box 210088, Tucson, AZ
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                                                                  Site_1: EcoRI; Site_2:
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Zhou, B., Mazur, E.,

EST 08-APR-2003

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Gaps

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REFERENCE AUTHORS

SOURCE ORGANISM

KEYWORDS VERSION ACCESSION DEFINITION RESULT 11 AA896321

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ORIGIN

Query Match Best Local ( Matches

COMMENT

TITLE JOURNAL

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RESULT 13
CB625990/c
LOCUS
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BJP602768646.R1 CSEQFXL38 p
CDNA, mRNA sequence.
BM659898.1 GI:18962904
EST.
Sus scrofa (pig)
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Oryza Bativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnollophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 822)
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BACKWARD: gga aac agc tat gac cat g
Plate: 15 row: O column: 13
Seq primer: gga aac agc tat gac cat
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between rice and Magnaporthe grisea Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E. Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
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                                                                                                      BM659898
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/mol_type="mRNA"
/cultivar="IR36"
                                                                                                                                                                                                                                                                                                              /clone lib="OSIIEa"
/note="Vector: pBluescript
XhoI; Lesion Mimic SPL 11"
                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:39946"
/clone="OSIIEa15013"
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                                                                                                                                                                                                                                                    70.6%;
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                                                                                                    365 bp
                                                                                      pig
                                                                                                                                                                                                                                                       36;
                                                                                        bp mRNA linear EST 27-FEB-2002
thyroid and parathyroid Sus scrofa
                                                                                                                                                                                                                                 DB 14; LC.
1.7e+02;
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                                                                                                                                                                                                                                                                  Length 822;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
                                                                                                                                                                                                                                                                     Immnology Department
Jiang Xi Medical College
106, Bayi Street, Nanchang, Jiangxi,
Tel: 86-0791-6363001
                                                                                                                                                                                                                                                                                                                                                                         lgG4 immunology screen 
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                Blattidae, Periplaneta.

1 (bases 1 to 378)
Zhou,Z.W., Liu,Z.G. and Gao,B.
The construction of Periplaneta americana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Hexapoda;
Neoptera; Orthopteroidea; Dictyoptera; Bl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pa002 Periplaneta americana Lambda Express library Periplaneta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: david.adelson@tamu.edu
Location/Qualifiers
                                                                                                                                                                                                                              Email: Zhouzhenwen28@hotmail
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                        Contact: Zhou, Z.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Periplaneta americana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Periplaneta americana (American cockroach)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Animal Science Dept., TAMU-2471, College Station,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ294503.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             americana cDNA clone 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 9798452616
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/note="Organ: thyroid and parathyroid gland; Vector:
pBluescript SK+; Site 1: Not1; Site 2: EcoRI; sequence 5
of the insert (5'-NNNT'...NNNinsert)
of cGAANTTGAAGCTCACCGCGGTGGCGGCGCTCAGG. Sequence 3' of
the insert (AAGAATTGAATTCAAGCTTATCGATACCGTGCACCTCGAG.
non-normalized library, sequenced 3' with M13R primer."
    screened
/clone lib="Periplaneta americana Lambda Express library"
/note="Vector: Lambda Excell; These sequences were
screened by cockroach sensitive patients' IgG4 serum "
                                                              /tissue_type="whole body"
/dev_stage="nymph"
/lab_host="E.coli_NM522"
                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:6978"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                   organism="Periplaneta americana"
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Dictyoptera; Blattaria; Blattoidea;
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BI961415
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Best Local (
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                                                                                                                                                               139
                                 sequence.
BI961033
                                                  81961033 446 b
MONO1_5_C04.b1_A005 Monocytes
                                                                                                                                                                     1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGAA 45
               BI961033.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence: 20. Three-prime sequences, which are obtained with PolyTMix or Tequencing primer, are presented as the reverse complement.
                                                                                                                                                ĠĀĠĠĀTĠĀĀĠĀTĠĀĠĠĀĠĠĀĀĠĠĀĀĠĠĀĀĠĠĀĠĠĀĠĀĠŢĠĀĀ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vandenplas,M.L., Cordonnier-Pratt,M.-M., Sudman,M.L., Gingle, A.R., Pratt,L.H. and Moore,J.N. An EST database from equine (Equus caballus) monocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
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EST.
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MONO1_5 C04.91_A005 Monocytes
sequence
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                                                                                                                                                                                                                                                                                /organism="Equus caballus"
/mol_type="manua"
/mol_type="manua"
/db xref="taxon:9796"
/db xref="taxon:9796"
/cell_type="Isolated peripheral blood monocytes stimulated with E. coli lipopolysaccharide"
/clone_lib="Monocytes (MONOI)"
/note="Wector: palluescript SK(-) from Lambda ZapII;
Site_1: XhoI, Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAPII. Clones to be sequenced were prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
            GI:16319236
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                                                                                                                                                                                                                                     69.4%;
86.7%;
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86.7%;
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                                                                                                                                                                                                                              Score 35.4; DB 12;
Pred. No. 2e+02;
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Pred. No. 2e+02;
                                                446 bp mRNA linear |
Ytes (MONO1) Equus caballus
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                                                              EST 22-OCT-2001
                                                  CDNA, mRNA
                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139
                                                            MRC Human Genome Mapping Project
Hinxton, Cambridge, CB10 1SB, UX
Email: biohelp@hgmp.mrc.ac.uk
Vector: pME185-FL3
                                                                                                                                             Takifugu rubripes ESTs
Unpublished (2002)
Contact: Clark MS
                                      V_type: phagemid
PRIMER: ME-735FW
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetradontoidea; Tetradontoidea; Tetradontidae; Takifugu.
                                                                                                                                                                                                                                                                                                              Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
          ibrary created by Koichi Kawakami,
                                                                                                                                                                                                         Clark, M.S.
                                                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                                                                  AL842491 F000H Takifugu rubripes cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                                                                                                                                                                                                                                                                                        AL842491.1 GI:22020319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmpratterig.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for high quality sequence:
20. Three-prime sequences, which are obtained with PolyTMix or T:
sequencing primer, are presented as the reverse complement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAĞĞATGAAĞATĞAĞGAĞĞAĞĞAAĞAĞAĞAĞĞAĞĞAĞAĞTĞAA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant
Plant Sciences Building, Rm. 2502, Athens, GA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalla; Butheria; Perissodactyla; Equidae; Equus.

1 (bases 1 to 446)

Vandenplas, M.L., Cordonnier-Pratt, M.-M., Sudman, M.L., Wentzel, V.E (dingle, A.R., Pratt, L.H. and Moore, J.N.

An EST database from equine (Equus caballus) monocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Equus caballus
Equus caballus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Equus caballus"
/mol_type="mRNA"
/db_xref="taxon:9796"
/db_xref="taxon:9796"
/cell_type="Isolated peripheral blood monocytes stimulated with E. coli lipopolysaccharide"
/clone_lib="Monocytes (MONOl)"
/note="Wector: pBluescript SK(-) from Lambda ZapII;
Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAPII. Clones to be sequenced were prepared by mass excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (horse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35.4; DB 12;
Pred. No. 2e+02;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 447
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                                                                                                                      Resource
Masahide Sasaki, Yutaka Suzuki,
                                                                                                                                                                                                                                                                                                                                                                                                                linear EST 30-JUL-2002
e F000H05aE11, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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GA 30602-7271,
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AW760336
LOCUS
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VERSION
KEYWORDS
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                                                    FEATURES
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                                                                                             Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, U
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further in
call: (800)-533-4363 or contact via email: ccu@resgen.com
Insert Length: 1134 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                    Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Bowers, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW760336 496 bp mRNA linear EST 03-DEC-2001 8149a06.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-4619 5' similar to TR:082214 082214 T29E15.4 PROTEIN.;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory of Aquatic Molecular Biology and Biotechnology, Graduat. School of Agricultural and Life Sciences, The University of Tokyo, Bunkyo-ku, Tokyo 108-8639, Japan Library sequenced by Melody S. Clark and Amanda Thompson MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine max
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AW760336.1 GI:7692223
EST.
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                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Institute of Medical Science, The University of Tokyo Shirokanedai, Minato-ku, Tokyo 108-8639, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 496)
                                                                             quality sequence stop: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:31033"
/clone="F000H05aE11"
organism="Glycine max"
                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Vector: pME18S-FL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/clone_lib="F000H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Takifugu rubripes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="heart"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.4; DB Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watabe
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                                                                                                                                                       information
                                                                                                                                                                                                                                                                                              USA
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CB272922/c
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KEYWORDS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        512 bp mRNA mai64007.yl McCarrey Eddy spermatocytes IMAGE:6446341 5', mRNA sequence CB272922
                                                                                                                                                                                                                           1 (bases 1 to 512)
MCCarrey,J., Eddy,M., Marra,M., Hillier,L., Clifton,S., Pape,D.,
Martin,J., Wylie,T., Dante,M., Bowers,Y., Theising,B., Gibbons,M.,
Ritter,E., Tsagareishvili,R., Ronko,I., Maguire,L., Kennedy,S.,
Bennett,J., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
Tel: 314 286 1800
Fax: 314 286 1810
                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St.
                                                                                                                NIEHS Mouse
                                                                                                                                                                     Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CB272922
CB272922.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAAC 46
                                                                                                                                           Contact: McCarrey/Eddy NIEHS Mouse
                                                                                                                                                                                                      NIEHS Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthesize the cDNA. First- stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGAGACTAGTCTCGAG(T)18] to anchor the primer at the 5' end of the poly(A) tract. After second- strand synthesis, the cDNA ends were filled in with cloned by the singented. The CNA solution the first-strand synthesis primer was then restricted by digestion with XhOi, all XhOI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRI Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated vector (pBluescript II SX(+) that has been digested with ECORI and XhOI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=30). This library was constructed by Dr. Paul Keim and Dr. Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI, This cDNA library was constructed from mRNA isolated
from cotyledons of 3- and 7-day-old_Williams_seedlings
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seedlings"
/lab_host="DH10B"
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/tissue_type="cotyledons of 3- and 7-day-old Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                           Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                              MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 24-FEB-2003
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CF795982/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phoromore with the aid of the trim_alt option.
Plate: TMW8018 row: D column: 17
                                                                                                                                                                                                                             Contact: Smith TPL
USDA, ARS, US Meat Animal
PO Box 166, Clay Center, 1
                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 552) Snith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W. Porcine BST collection using a normalized library constructed from embryos representing early developmental stages
                                                                                                                                                                             Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CF795982 552 bp mRNA linear 892192 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF795982.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 86.7
39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library constructed and donated by J. McCarrey, Ph.D. (Southwest Foundation for Biomedical Research, Dept. of Genetics) - excision done by E.M. Eddy, Ph.D. (National Institutes of Health, National Total Control of Contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seg primer: Primer name ambiguous
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Institute of Environmental Health Sciences)
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/clone lib="McCarrey Eddy spermatocytes"
/ste library vector: pBluescript SK+
(Stratagene); Site 1: XhoI; Site 2: EcoRI; cDNA oligo
dT.primed [5'-(GA)Io-ACTAGTCTCGAGTTTTTTTTTTTTTT-3'] and
and 5'-CTCGTGCCG-3'. Size selection of >400bp material
and 5'-CTCGTGCCG-3'. Size selection of >400bp material
mass excised (from lambda-UniZAF-XR) and resulting
into pH10B. Library contains 98% recombinants.

Eibrary constructed and donated by J. McCarrey, Ph.D.
Genetics); excision done by E.M. Eddy, Ph.D. (National
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63422."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:37800555
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/mol_type="mRNA"
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ne_lib="McCarrey Eddy spermatocytes"
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column: 17
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Pred. No. 2.1e+02;
0; Mismatches 6;
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                                                                                                                                                                                                                         Research Center
NE 68933-0166, USA
                                                                      phred v0.020425.c and
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BX669429
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Tel: 33 (0) 5.61.28.51.14
Fax: 33 (0) 5.61.28.51.08
Email: tosser@toulouse.inra.fr
Clone distribution: AGENAE Resource centre. François PIUMI, genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33 (0) 1.34.65.22.73
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this secures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 0031 row: e column: 12.
Location/Qualifiers
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1 (bases 1 to 556)
Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soares, M., Bonaldo, F. and Hatey, F.
A Pig Normalised Multi-Tissue cDNA Library
Contact: Tosser-Klopp G
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Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (pig)
Sus scrofa
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/mol_type="mRNA"
/db xref="taxon:9823"
/clone="scac0031i.e.12"
/clone="scac0031i.e.12"
/clone="scac0031i.e.12"
/clone lib="Gus Scrofa library (scac)"
/clone lib="Sus Scrofa library (scac)"
/note="Wector: pT713D-pac vector; tissues: adipose tissue, brain, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, nate of the process of the proc
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mol_type="mRNA"
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/lab_host="DH10B"
/clone_lib="MARC_4PIG"
/clone_lib="MARC_4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/ibrary made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
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/db_xref="taxon:9823"
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86.7%;
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Pred. No. 2.1e+02;
0; Mismatches 6
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AI451753 586 bp mRNA linear mb16f09.y1 Soares mouse p3NMF19.5 Mus musculus cDNA IMAGE:329609 5' similar to TR:Q12804 Q12804 RECEPIN.
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BX676418
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Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
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Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Vill soares, M., Bonaldo,F. and Hatey,F.
A pig Normalised Multi-Tissue CDNA Library Unpublished (2003)
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BX676418
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33 (0) 5.61.28.53.08
1: tosser@toulouse.inra.fr
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                                                                                                                                                                                                                                                                                                                        /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="scac00311.e.12"
/clone="scac00311.e.12"
/clone lib="Sus Scrofa library (scac)"
/clone lib="Sus Scrofa library (scac)"
/clone lib="Sus Scrofa library tissues: adipose tissue, /note="Vector: pT773D-pac vector; tissues: adipose tissue, /note="Vector: pt773D-pac vector; tissues: adipose tissue, /note, kidney, liver, muscle, ovary, testis, heart, hypothalamus, pancreas, skin, spleen, thymus, placenta, pituitary gland, seminal vesicle, small intestine, uterus, adrenals, bulbo uretral gland, cerebral trunk, epididymis, female gonad, gall-bladder, hippocampus, large intestine, male gonad, melanocytes, stomach, udder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRANCE
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86.7%;
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                                                                                                                                                                                                                        Score 35.4; DB 13;
Pred. No. 2.1e+02;
0; Mismatches 6;
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                       clone
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                                        EST 15-MAR-2000
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Best Local
                                                               ORGANISM
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Marra,M., Hillier,L., Kucaba,T., Martin,Junderwood,K., Steptoe,M., Theising,B., Al Person,B., Swaller,T., Gibbons,M., Pape,I Ritter,E., Kohn,S., Shin,T., Jackson,Y., Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                       CF367914
852497 MARC 3PIG
CF367914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39;
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AI451753.1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                            Sus scrofa (pig)
Sus scrofa
                                                                                                                           CF367914.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the content of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          correct orientation)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:329609"
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                                                                                                                                                             GI:34172915
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                                                                                                                                                                                                                         Sus scrofa
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Pred. No. 2.1e+02;
0; Mismatches 6
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                                                                                                                                                                                                                      6 bp mi
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   Euteleostomi;
Sus.
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; Murinae; Mus
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CF792336/c
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Best Local !
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                                                                                                          Cross match v0.990329.
Plate: TMW8012 row: I
                                                                                                                             Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified of the trim_alt option.
                                                                                                                                                                                                                                                  Manmalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 673)

Smith, T. P. L., Freking, B.A., Ford, J.J., Vallet, J.L., Wise, T.A.,

Nonneman, D.J., Wray, J.E. and Keele, J.W.

Porcine EST collection using a normalized library constructed from Unpublished (2003)

Contact: Smith TPL

Torn TRO
                                                                                                                                                                        Email: smith@email.marc.usda.gov
                                                                                                                                                                                                 Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                        USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, UK
                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (pig)
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CF792336
CF792336.1 GI:37796897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF792336 673 bp mRNA linear
885253 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGAA 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross match v0.990329.
Plate: SRG8023 row: J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 402 762 4366
Fax: 402 762 4390
                                                                                     te: TMW8012 row: I column: 1
primer: TAGAAGGCACAGTCGAGG.
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Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Wise, T.A., Nonneman, D.J., Wray, J.E. and Keele, J.W.
A second set of porcine ESTs from a pooled-tissue normalized library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="pooled"
/lab host="DHIOB"
/clone_lib="MARC 3PIG"
/clone_lib="MARC 3PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
/inbrary made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."
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/mol_type="mRNA"
/db_xref="taxon:9823"
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Pred. No. 2.1e.
0; Mismatches
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                                                                                                                                                         COMMENT
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AUTHORS
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BY706040/c
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VERSION
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VERSION

TITLE

FEATURES

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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Fletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Nonagaya, A., Mumata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Read, D.J., Reid, J., Ring, B.L., Konagaya, A., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Washaw-Boria, A., Yangisawa, M., Yangi, L.G., Wilming, L.G., Wynshaw-Boria, A., Yangisawa, M., Yangi, I., Hayatsu, N., Sato, K., Shiraki, T., Maki, K., Kawai, J., Aizawa, K., Yangis, Of, the mouse transcriptome based on functional annotation Malure 420, 563-573 (2002)
              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., /
Fukuda,S., Hashizume,W., Hayashida
                                                                                                                         1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                               Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 GAGGAGGAAGATGAGGAGGAGGAAGAAGAAGAAGAGAGTGAA 130
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BY706040 RIKEN full-length enriched,
CDNA clone 1700012D21 5', mRNA seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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/lab host="DH108"
/lab host="DH108"
/clome lib="MARC 4PIG"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: Not!
Library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."
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Pred. No. 2.2e+02;
"'smatches 6; Indels
     imura, T., Arakawa, T., Carninci
Hayashida, K., Hirozane, T., Ho
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d, adult male testis Mus musculus
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nci, P.,
Hori, F.,
                                                                                                                                                     230-0045, Japan
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genomic survey sequend
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
                                                                                                                                                                                                                                                                                                                              μ
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                                                                                   BZ504700.1 GI:27024259 GSS.
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                                                              Brassica oleracea
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/db_xref="taxon:10090"
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86.7%;
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishih,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384 format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                           Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1080 bp mRNA linear HTC 20-SE
Mus musculus adult male testis CDNA, RIKEN full-length enrich
library, clone:1700012D21 product:similar to CBF1 INTERACTING
COREPRESSOR CIR [Homo sapiens], full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
Other GSSs: BONRX59TF
                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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Class: sheared ends.
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Chris Town
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1 (bases 1 to 823)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
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DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whole genome shotgun sequencing of Brassica oleracea
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/note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared total DNA inserted into pHOS1 using BstXI linkers"
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/strain="TO1000DH3"
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Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Hiraoka, T., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Jahi, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, Y., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Tejima, Y., Toya, T., Yasunishi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Yoshida, K., Direct Submission
1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAA 45
                                                          39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, Fax:81-45-503-9216)
Fax:81-45-503-9216;
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                  Conservative
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                                                                    Submitted (10-UL-2000) Yoshihide Hayashizaki, The Institute chysical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The RIKEN Genome Exploration Research Group Phase II Team and
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010015A19 product:similar to CBF1

INTERACTING COREPRESSOR CIR [Homo sapiens], full insert sequence.
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APPLICANT: Junice Au-Young
APPLICANT: Junice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION

OUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMMUNICATION OF SIGNALIA CONTRY OF STATES CALIFORNIA
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1534
1824
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US-09-614-124B-316
US-09-671-325-316
US-09-671-325-316
US-09-671-325-78
US-09-671-325-78
US-09-671-325-78
US-09-89-184-40
US-09-68-314-309A-1
US-08-800-971-3
US-08-800-971-1
US-08-800-971-1
US-08-800-971-3
US-08-81-86-209
US-09-68-11-66-209
US-09-68-419-11
US-08-81-464-13
US-09-733-458-3
US-09-733-458-3
US-09-733-458-3
US-09-800-933-15
US-09-
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US-08-935-855-21

US-08-935-855-21

US-09-894-998A-35

US-08-785-420-1

US-09-72-032-8

US-09-443-218-8

US-08-630-915A-195

US-09-620-312D-761

US-09-580-3830-17

US-09-620-312D-106
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US-09-702-705-788
US-09-736-457-316
US-09-736-457-788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 5, Appli Sequence 5, Appli Sequence 209, App Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 17, Appli Sequence 17, Appli Sequence 15, Appli Sequence 11, Appli Sequence 11, Appli Sequence 13, Appli Sequence 14, Appli Sequence 15, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 18, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 17, Appli Se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e 40, Appl
e 18762, A
e 10, Appl
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Strong, Theresa
APPLICANT: Conry, Robert M.

APPLICANT: LoBuglio, Albert F.

ITILE OF INVENTION: Melanoma Antigens and Methods of Use
FILE REFERENCE: D6253
CURRENT APPLICATION NUMBER: US/09/691,538A
CURRENT FILING DATE: 2000-10-18
PRIOR APPLICATION NUMBER: US 60/160,042
PRIOR APPLICATION NUMBER: US 60/160,042
INUMBER OF SEQ ID NOS: 12
SEQ ID NO 12
FENORUL EGG
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
ILBRARY: GENBANK
CLONE: 9178197
US-09-016-434-1181
                                                                                                                                                                                                                                      US-09-691-538A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-691-538A-12

; Sequence 12, Application US/09691538A

; Patent No. 6677444
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                                                                                                                                         Matches
                                                                                                                                                                       Best
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                   LENGTH: 593
TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                           PEATURE:
OTHER INFORMATION: 3' end of clone 5.31 encoding
OTHER INFORMATION: tumor-associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
                                                                                                                                                                  Local
                                             295
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                                                                                                                                         42;
                                                                                                                                                          Similarity
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                      GĀĞGĀGGĀGGAAGĀTGĀGGĀGGĀCGĀGGĀĀGĀĀGĀĀGĀĞĀĞTGĀĀCCTCĀĞ 345
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91.7%;
                                                                                                                                                   71.8%;
82.4%;
                                                                                                                         Score 36.6; DB
Pred. No. 0.033;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41.6;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEPAX: (609) 779-9488
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                tent No.
                                                                                                                      APPLICANT: Kahn, C. Ronald
APPLICANT: White, Morris F.
APPLICANT: Rothenberg, Paul Louis
TITLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/176,218
FILING DATE: December 30, 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/114,951
FILING DATE: August 31, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb
MEDIUM TYPE: STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: David S. Strayer and Avinash Chander
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Targeting Cells and Modulating Pulmonary Surfactant Secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: JEFF-0042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 210 Lake CITY: Cherry Hill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
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                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                              Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
EDNESS: single stranded
                                                                                                                                                                                                                                                                                                                                                                                                                              GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jane Massey Licata
                                                                                                                                                                                                                                                                                               Application US/08094948A
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                                                                        Massachusetts
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                                                                                                               60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Jane Massey Licata, Esq.
210 Lake Drive East, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                       U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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88.4%; Pred. No. 0.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application:
                                                          APPLICATION NUMBER: PCT/US96/09319
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/094,948
FILING DATE: 21-UUY-1993
APPLICATION NUMBER: US 07/643,982
FILING DATE: 18-UAN-1991
ATTORNEY/AGENT INFORMATION:
ANALYSIS (PLM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
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REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JD:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 18-JAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: 1BM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Lahive & Cockfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                      NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                PLICANT: White, Morris F.
PLICANT: Rothenberg, Paul Louis
TLE OF INVENTION: INSULIN RECEPTOR SUBSTRATE
                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Myers, Louis (PLM)
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application PC/TUS9609319
                                                                                                                                                                                                                                                                                                                                                             Boston
                                                                                                                                                                                                                                                                                                                            Massachusetts: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                               60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5125 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kahn, C. Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                         Floppy disk
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                                                                                                                                                                                            PCT/US96/09319
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                        JDP-013DV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.2; DB Pred. No. 0.19; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JDP-013DV
                                                                                                                                                                                                                             Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

4.

ENGTH:

H: 5125 base pairs nucleic acid DEDNESS: single

STRANDEDNESS: sing TOPOLOGY: linear MOLECULE TYPE: cDNA

PCT-US96-09319-4

NAME/KEY:

CDS 589..4053

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US-09-621-976-18769
; Sequence 18769, Application US/09621976
; Patent No. 6639063
                                                                                                RESULT 7
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                                                                                                                                                                                                                                                                    US-09-328-111-333
                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NOVEL HUMAN GENES AND GENETATION OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
FEARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1988-06-10
   GENERAL INFORMATION:
APPLICANT: Dumas Mi
APPLICANT: Jobert,
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(650)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                       Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASUSEQ for Windows Version 3.0
SEQ ID NO 333
LENGTH: 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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APPLICANT: Catino, Theodore J
APPLICANT: Derti, Adnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Steinmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT: Burgess, Christopher C. PPLICANT: Bushnell, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                            245
                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAACCCC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333,
                                                                                                                                                                                                                   Similarity
Dumas Milne Edwards, J.B. Jobert, S.
                                                                                                                         ĠĀĠĠĀĠĠĀĠŖĀĠŖĀĠĀĀĠĀĠĠĀĠĠĀĠĠĀĠĠĀĠĠĀĠĠĀĠŖĀĠĀĀĀĊŖĊ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/09328111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theodore J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson O
                                                                                                                                                                                                                  79.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kathleen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.1%;
83.0%;
                                                                                                                                                                                          Score 33; DB 3;
Pred. No. 0.34;
0; Mismatches
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Pred. No. 0.19;
0; Mismatches 8;
                                                                                                                                                                                                                       DB 3; Length 650;
                                                                                                                                                                                          10; Indels
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; Sequence 34, Application US/09894998A
; Patent No. 6537555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/894,998A
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 34
LENGTH: 661
TYPE: DNA
ORGANISM: HSV-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
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                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                          -09-620-312D-1085
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Best Local S
                                                       PPLICANT
                                                                                    PPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hosken, Nancy Ann
APPLICANT: Craig H. Day
APPLICANT: Craig H. Day
APPLICANT: Davin C. Dillon
APPLICANT: McGowan, Patrick
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION
FILE REFERENCE: 210121.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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LENGTH: 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENERY 1054PR2.

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: PACENT.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 89.7
les 35; Conservative
                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                1085, Application US/09620312D
>. 6569662
                                                                                                                                                                                                                                                                                                                               42 GAGGAGGAGGCGGAAGAGGAGGAGGAGGCGGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 GAGGAAGAAGGTGGGGAGGAAGAAGAAGGAAGAAGAATGTGA 391
                                                                                                                                                                                                                                                                                                                                                    1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                            Tang,
Liu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGAGAGTGTGA 44
                                                                                           Liu, Chenghua
Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
                                              Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
Wang, Jian-Rui
Ma, Yunging
Wang, Dunrui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n 64.3%;
Similarity 84.1%;
37; Conservative
                                Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                               63.9%;
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Pred. No. 0.44;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 661;
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APPLICANT: Drmanac, Radoje T.

ITITLE OF INVENTION: No. 65696221 Nucleic Acids and

ITITLE OF INVENTION: Polypeptides

FILE REFERENCE: 784CIP2B

CURRENT FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR APPLICATION NUMBER: 09/552,317

PRIOR PILING DATE: 2000-04-25

PRIOR PILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: pt_FL_genes Version 1.0

SEQ ID NO 1085

LENGTH: 2817
                                                                                                         RESULT 11
US-09-702-705-1668
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (109)..(2817)
US-09-620-312D-1085
                                                                                                                                                                                                                                                                                                                                                                   US-09-392-714-1
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/392,714A
CURRENT FILING DATE: 1999-09-09
EARLIER APPLICATION NUMBER: PCT/US98/14679
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
                                       Sequence 1668, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09392714A Patent No. 6686147 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Cancer Associated Antigens and Uses TITLE OF INVENTION: Therefor FILE REFERENCE: L0461/7062
                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 14561
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                           6252 GAGGAGGAAGATGAGGAGGAGGAGGAAGAAGAGAGAGTGAA 6296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209 AGGGTGAGGAGGAAGAGGAGGAAGAGAGGAAGAGAGGATGACC 253
                                                                                                                                                                                                                                                                               37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                              GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGAA
Wang, Tongtong
Bangur, Chaitanya S.
                                                                                                                                                                                                                                                                             63.1%;
ilarity 82.2%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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US-09-614-124B-1668

Sequence 1668, Application US/09614124B Patent No. 6630574

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong APPLICANT: Bangur, Chaitanya S.

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SOFTWARE: FastSEQ for Wi
SEQ ID NO 1668
LENGTH: 636
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-1668
                                                                                                                                                                                        ; SOFTWARE: FASTSEQ for Wi
; SEQ ID NO 1668
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1668
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RESULT 13
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                                                                                                                        Matches
                                                                                                                                     Query Match
Best Local Similarity
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 62.4%;
Local Similarity 76.5%;
hes 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            586 GAGGAGGAAGAAGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636
                                                   586 GAGGAGGAAGAAGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636
                                                                                                                      39;
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                                                                                  1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCAG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 3.0
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Retter, Marc
Mannion, Jane
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Retter, Marc
Mannion, Jane
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Vedvick, Tom
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Bangur, Chaitanya
Lodes, Michael A.
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Vedvick, Tom
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                                                                                                                        Conservative
                                                                                                                                       76.5%;
                                                                                                             ; Score 31.8; DB; Pred. No. 0.74; O; Mismatches.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31.8; DB Pred. No. 0.74; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                        12;
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Fanger, Gary Vedvick, Tom

Lodes, Michael A.

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APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION UNMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
SOFTWARE: FASESEQ ID NOS: 1668
SOFTWARE: FASESEQ for Windows Version 3.0
LENGTH: 636
TYPE: DNA
ORGANISM: Homo sapiens
US-09-614-124B-1668
                                                                                                                                                                                                                                                                                                                             APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOF
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671,325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1668
                                                                                                                       US-09-345-882-21
                                                                                                                                         RESULT 15
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                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-671-325-1668
                                                      Sequence 21, Application US/09345882
Patent No. 6399373
GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
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Best Local
            FILE REFERENCE: GENSET.031A
                              TITLE OF INVENTION: ANI
                                                                                                                                                                                                                                             Matches
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Patent No. 666715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                            586 GÁGGAGGAAGAAGAGGAGGAGGAGGAGGAGGATGAATAATGACTCGAG 636
                                                                                                                                                                                      1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAGTGTGAACCCCAG 51
                                                                                                                                                                                                                                         39;
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                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bangur, Chaitany
Lodes, Michael A
Fanger, Gary
Vedvick, Tom
Carter, Darrick
Retter, Marc
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Fan, Liqun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang,
                                                                                                                                                                                                                                     Conservative
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et, Lydie
A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
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                                                                                                                                                                                                                                                62.4%;
76.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chaitanya S.
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                                                                                                                                                                                                                                   0;
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Pred. No. 0.74;
0; Mismatches 12; Indels
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US-08-574-959A-8
                                         Query Match
Best Local Similarity 85...
34; Conservative
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LENGTH: 258

TYPE: DNA

ORGANISM: Homo sapiens
US-09-345-882-21
                                                                                                                                                                                                                                                                                                   COMPUTER REALIGHER FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/574,959A
APPLICATION NUMBER: US/08/574,959A
ATTORNBY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 3211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear.
                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ
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Best Local S
                                                                                                                                                           MOLECULE TYPE: c
FEATURE:
NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/345,882 CURRENT FILING DATE: 1999-06-30 PRIOR APPLICATION NUMBER: US 60/091,315 PRIOR FILING DATE: 1998-06-30 PRIOR APPLICATION NUMBER: US 60/111,909 PRIOR FILING DATE: 1998-12-10 NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES, TITLE OF INVENTION: AND USES THEREFOR
                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDRESSEE:
1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGA
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5. 5962224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boston
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Similarity 89.5%;
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(617)227-5941
---- TD NO: 8:
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                                                                                                                                         439..3157
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                                                                        62.0%;
89.5%;
                                                 Score 31.6; DI
Pred. No. 0.96
0; Mismatches
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Pred. No. 0.77;
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                                                                             DB 2; Length 3211;
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RESULT 18
US-08-574-959A-6
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US-09-357-014-8
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Patent No. 6291645
GENERAL INFORMATION:
APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
and Jack L. Strominger
TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
AND USES THEREFOR
                                                                                                                                                                                                  Sequence 6, Application US/08574959A Patent No. 5962224
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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GRUBRAL INFORMATION:

APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger

TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES

TITLE OF INVENTION: AND USES THEREFOR

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSE: LAHIVE & COCKFIELD

STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/357,014
APPLICATION UNMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION UNMBER: 08/574,959
PRIOR APPLICATION UNMBER: 08/574,959
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 439. 3157
SEQUENCE DESCRIPTION: SEQ ID NO:
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LENGTH: 3211 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                 2590 GAGGAAGAAGAAGAGGAGGAGGAGGAGGAAGA 2627
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                                                                                                                                                                                                                                                                                                                                                                                                                     34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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LOCATION: 439
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                       62.0%;
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US-09-357-014-6
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Matches
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LOCATION:
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Sequence 6, Application US/09357014 Patent No. 6291645 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,20
REFERENCE/DOCKET NUMBER: 1
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                                FILING DATE: 19-Jul-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/574,959
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: MANGIAGOUIAS, Amy E.
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
mes 34; Conserv
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                                                                                                                                                                    SOPTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/357,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, AND USES THEREFOR
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: DFN-008 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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(617)227-5941
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ilarity 89.5%;
Conservative
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439..3847
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TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

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FEATURE:
NAME/KEY: CDS
LOCATION: (1)
US-09-620-312D-480
                                                 Query Match
Best Local Similarity 89.5
                                                                                                                                                             NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_Ft_genes Version 1.0
SEQ ID NO 480
LENGTH: 4226
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/620,312D CURRENT FILING DATE: 2000-07-19 PRIOR APPLICATION NUMBER: 09/552,317 PRIOR FILING DATE: 2000-04-25 PRIOR APPLICATION NUMBER: 09/488,725 PRIOR FILING DATE: 2000-01-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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APPLICANT:
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658 GATGAAGAAGCAGAAGAGGAGGAGGAGGAAGAAGA 695
                       1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGA
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LOCATION: 439..3847
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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Ren, Feiyan
Chen, Rui-hong
C: Zhao, Qing A.
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34; Conserv
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Ma, Yunqing
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Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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89.5%;
                                                  Score 31.6; DB 4;
Pred. No. 0.99;
0; Mismatches 4;
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Pred. No. 0.98;
0; Mismatches 4;
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FEATURE:
NAME/KEY: allele
LOCATION: 1315..1336
OTHER INFORMATION: 1
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US-09-345-882-4
        PEATURE:
NAME/KEY: allele
LOCATION: 1921..1967
OTHER INFORMATION: polymorphic fragment 5-136-174 SEQ ID62
                                                                        NAME/KEY: allele
LOCATION: 1921..1967
OTHER INFORMATION: po
                                                                                                                             NAME/KEY: allele
LOCATION: 1315..1338
OTHER INFORMATION: po
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LOCATION: 1107..1125
OTHER INFORMATION: po.
NAME/KEY: allele
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SEQ ID NO 4
LENGTH: 6002
                                                                                                                       FEATURE
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NAME/KEY: allele
LOCATION: 1338
OTHER INFORMATION: 5
FEATURE:
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Patent No. 63777.
Patent INFORMATION:
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LOCATION: 1107..1125
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Patent No. 6399373
                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: 5-148-352
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PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 3346
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
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LOCATION: 1319
OTHER INFORMATION: 5-130-257
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LOCATION: 3329
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.ON: polymorphic fragment
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                                                                                                                        polymorphic fragment
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NAME/KEY:
LOCATION:
                                           LOCATION: 818..1306
OTHER INFORMATION: complement
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LOCATION: 3323..3369
OTHER INFORMATION: polymorphic
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LOCATION: 3323..3369
OTHER INFORMATION: polymorphic
                                                              NAME/KEY: misc_feature
LOCATION: 818..1306
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OTHER INFORMATION: homology
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OTHER INFORMATION: potential
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OTHER INFORMATION: polymorphic
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LOCATION: 453..898
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LOCATION: 4378..4380
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LOCATION: 442.444
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OTHER INFORMATION: po
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OCATION: 5896..5901
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OTHER INFORMATION: polymorphic
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INFORMATION: po
INFORMATION: complement homology
              misc_feature
844..1303
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5981..5986
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 embl: AA262427
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                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                   Sequence 1, Application US/09345882 Patent No. 6399373
                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
           CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US 60/111,909
PRIOR FILING DATE: 1998-12-10
                                                                                              APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH
FILE REPERENCE: GENSET 031A
NUMBER OF SEQ ID NOS: 140
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LOCATION: 1351..1702
OTHER INFORMATION: complement homology
FEATURE:
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LOCATION: 5580..6002
OTHER INFORMATION: complement
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OTHER INFORMATION: homol
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LOCATION: 2253..2482
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LOCATION: 2181..2281
OTHER INFORMATION: home
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LOCATION: 4516..5016
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LOCATION: 3883..4221
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LOCATION: 3631..3870
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LOCATION: 3334..3733
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LOCATION: 2480..2842
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OTHER INFORMATION: homology
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LOCATION: 1866..2109
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ENGTH: 162450

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FEATURE:
NAME/KEY: allele
LOCATION: 134134
OTHER INFORMATION:
                NAME/KEY: allele
LOCATION: 134374
OTHER INFORMATION:
                                                LOCATION: 134362
OTHER INFORMATION:
FEATURE:
NAME/KEY: allele
                                                           NAME/KEY: allele
LOCATION: 134362
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LOCATION: 108149
OTHER INFORMATION:
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NAME/KEY: allele
LOCATION: 108106
OTHER INFORMATION: 5
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OTHER INFORMATION:
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LOCATION: 108471
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NAME/KEY: allele
LOCATION: 106940
OTHER INFORMATION:
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LOCATION: 108308
OTHER INFORMATION:
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LOCATION: 99098
OTHER INFORMATION: 5
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NAME/KEY: allele
LOCATION: 97152
OTHER INFORMATION: 5
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LOCATION: 72794
OTHER INFORMATION: :
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THER INFORMATION:
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THER INFORMATION:
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LOCATION: 93714
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 97122
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LOCATION: 90842
OTHER INFORMATION:
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OTHER INFORMATION: 5-127-261
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FEATURE:
NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polyn
NAME/KEY: allele
LOCATION: 99094..99140
                        LOCATION: 99075..99121
OTHER INFORMATION: polymorphic
FEATURE:
                                              NAME/KEY: allele
LOCATION: 99075..99121
                                                                                    NAME/KEY: allele
LOCATION: 99075..99121
OTHER INFORMATION: pol
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PEATURE:

NAME/KEY: allele

- ~~aTION: 93690..93736

- ~~aTION: polymorphic fr
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NAME/KEY: allele
LOCATION: 97099..97145
PARATION: polymorphic fragment
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LOCATION: 97130..97177
OTHER INFORMATION: pol-
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NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic
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LOCATION: 93690..93
OTHER INFORMATION:
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OTHER INFORMATION: complement polymorphic
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LOCATION: 90819..90865
OTHER INFORMATION: com
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LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ
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OTHER INFORMATION: polymorphic fragment
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NAME/KEY: allele
LOCATION: 72771...72817
CHURD INFORMATION: polymorphic fragment 5-124-273
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LOCATION: 72771..72817
OTHER INFORMATION: polymorphic
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LOCATION: 160031
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 150329
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OTHER INFORMATION:
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LOCATION: 146345
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OTHER INFORMATION:
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                                                                                    polymorphic
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                            fragment 5-130-257 SEQ ID55
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                                                                             SEQ ID34
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OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35

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CURRENT APPLICATION NUMBER: US/09/817,310
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 09/230,247
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 2556
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-817-310-1
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Query Match
Best Local Similarity
Matches 38; Conserv
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                                                                                                                                                                                                                                            APPLICANT: Stewart, Mary
APPLICANT: Kozma, Sarah
APPLICANT: Thomas, George
TITLE OF INVENTION: Drosophila Melanogaster P70 S6 Kinase
FILE REFERENCE: 4-20971/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
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LOCATION: 106918..106966
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LOCATION: 103783..103828
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LOCATION: 103783..103828
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DTHER INFORMATION:
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THER INFORMATION: polymorphic
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LOCATION: 108084
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DRMATION: polymorphic
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                  61.6%;
77.6%;
 Score 31.4; DB Pred. No. 1.1; 0; Mismatches
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US-09-736-457-309/c
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US-09-702-705-309/c
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                                           SOFTWARE: Fa
SEQ ID NO 309
LENGTH: 129
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Best Local
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APPLICANT:
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                                                                                    CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
                                                                                                                                 APPLICANT: Wang, Aijun
TITLE OF INVENTION: CAMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
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TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (1)...(129)
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TYPE: DNA
ORGANISM: Homo sapien
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Carter, Darrick
Retter, Marc
                                                                         FastSEQ for Windows Version
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Retter, Marc
Mannion, Jane
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Lodes, Michael
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Vedvick, Tom
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Lodes, Michael
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Bangur, Chaitanya
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Vedvick, Ton
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i NAME/KEY: misc\_feature
; LOCATION: (1)...(129)
; OTHER INFORMATION: n = A,T,C or
US-09-736-457-309

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US-09-614-124B-309
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FILE REFERENCE: DIAGNOSIS OF LUNG CANCER CURRENT APPLICATION NUMBER: US/09/671,325

CURRENT FILING DATE: 2000-09-26
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SEQ ID NO 309
LENGTH: 129
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APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
NUMBER OF SEQ ID NOS: 1668
COFTWADER: Caster Seator For Wissian Number Caster For Wissian Numb
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Best Local Similarity
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LOCATION: (1)...(129)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, Tongtong
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Wang, Tongtong
Tongur, Chaitanya g
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Lodes, Michael
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Lodes, Michael A.
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CURRENT APPLICATION NUMBER: US/09/589,184
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 827
SOFTWARE: FastSEQ for Windows Version 3.0
ENGIT: 129
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(129)
US-09-589-184-309
US-09-589-184-309
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET: 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
                                                                                                                             GENERAL INFORMATION:
                                                                                                                                             Sequence 18731, Appeared No. 6639063
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C8
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ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(129)
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Similarity 81.8%;
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Carter, Darrick
Retter, Marc
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Bangur, Chaitanya
Lodes, Michael A.
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                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                     Application US/09621976
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Pred. No. 0.94;
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FRIERI NO. 00370001

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT PALING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PAtent.pm
SEQ ID NO 18711
LENGTH: 427
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 72,215,229
OTHER INFORMATION: n=a, 9, c or t
US-09-621-976-18711
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Search completed: February 29, 2004, 22:26:08 Job time: 65.5 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQ ID NO 18731
, LENGTH: 403
; TYPE: DNA
; ORGANISW: Homo sapiens
US-09-621-976-18731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18711, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 61.2%; Score 31.2; DB 4; Length 403; Best Local Similarity 81.8%; Pred. No. 1; Matches 36; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                  Query Match 61.2%; Score 31.2; DB 4; Length 427; Best Local Similarity 81:8%; Pred. No. 1; Matches 36; Conservative 0; Mismatches 8; Indels (
                                                                                             343 GAGGAAGAAGGTGGGGAGGAAGAAGAAGAAGAAGAAGGTGA 386
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Maximum Match 100%
Listing first 150:
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Perfect score:
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Maximum DB
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Match Length
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1 gaggatgaagctgaagagga.....aggaagagtgtgaaccccag
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          Copyright
          GenCore version (c) 1993 - 2004
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9 US-09-825-923-1

14 US-10-077-870-1

14 US-10-077-870-1

14 US-10-077-870-3

4 US-10-077-870-3

4 US-10-001-073-1

5 US-10-305-720-1181

4 US-10-125-567A-41

4 US-10-128-714-6204

1 US-10-128-714-204

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1 US-10-128-714-5204

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     Sequence 2, Appli
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             9 US-09-864-761-23094
10 US-09-918-995-27029
9 US-09-864-761-6378
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US-09-844-864-5

2 US-10-424-599-108927

5 US-10-369-493-27799

4 US-10-205-194-145
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i Sequence 2, Application US/10001073
i Publication No. US20030113725A1
i GENERAL INFORMATION:
i APPLICANT: Liggett, Stephen
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16 US-10-037-270-4480
17 US-10-137-722-480
18 US-01-126-704-4
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                                                                                                                                                    ALIGNMENTS
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Sequence 329, App
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Sequence 17651, Appli
Sequence 17651, Appli
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Sequence 17651, Appli
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Sequence 312, App
Sequence 9110, App
Sequence 111, App
Sequence 606, App
Sequence 1309, App
Sequence 9881, Ap
Sequence 103743,
       RESULT 3
US-10-077-870-1
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                                                                                                                                                            Query Match
Best Local S
Matches 49
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US-09-825-923-1
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TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
CURRENT APPLICATION UNMERE: US/10/001,073
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1344
TYPE: DNA
CTANNOW: "Inc. carian."
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Best Local
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GENERAL INFORMATION.

APPLICANT: Snapir, Amir
APPLICANT: Heinonen, Paula
APPLICANT: Heinonen, Paula
APPLICANT: Alhopuro, Pia
APPLICANT: Karvonen, Matti
APPLICANT: Karvonen, Matti
APPLICANT: Koulu, Markku
APPLICANT: Koulu, Markku
APPLICANT: Scheinin, Mika
APPLICANT: Scheinin, Mika
APPLICANT: Lakka, Timo A
APPLICANT: Nyyss"nen, Kristiina
APPLICANT: Kauhanen, Jussi
APPLICANT: Valkonen, Veli-Pekka
TITLE OF INVENTION: A DAA molecule encoding a variant alpha-2B-adrenoceptor
FILE REFERENCE: Alpha-2B-AR variant
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR FILING DATE: 2000-05-25
RUMBER OF SEQ ID NOS: 10
SEQ ID NO 1
LENGTH: 1344
TYPE: DNA
; Sequence 1, Application US/10077870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens US-10-001-073-2
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Patent No. US20010016338A1
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAMS/KEY: CDS
LOCATION: (1)..(1341)
OTHER INFORMATION: Coding sequence for variant human
OTHER INFORMATION: alpha-2B-adrenoceptor protein
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                                                                                                                                                                                                                      93.7%;
96.1%;
                                                                                                                                                                                            Score 47.8; DB 9;
Pred. No. 9.5e-06;
0; Mismatches 2
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RESULT 5
US-09-825-923-3
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PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN VET. 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 47
LENGTH: 6904
                                                                                                                                                Matches
                                                                                                                                                                                Query Match
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Best Local Similarity
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TITLE OF INVENTION: Method for detecting a
FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune TITLE OF INVENTION: cytosine methylation FILE REFERENCE: 5013.1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OLEK, APPLICANT: PIEPE
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                                                                                                                                                                                                                                                       NAME/KEY: unsure
LOCATION: 6084
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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OTHER INFORMATION: Coding sequence for variant human alpha-2B-adrenoceptor protein
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                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: chemically treated genomic
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                                                                                                                                                                 Local Similarity
                                                                         5880
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                                                                                                             1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGTGTGAA 45
                                                                         GAGGATGAAGTTGAAGAGGAGGAGGAGGAAGATTGTGAA 5924
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No. US20030143606A1
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96.1%;
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Pred. No. 9.5e
0; Mismatches
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Pred. No. 0.00064;
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                                                                                                                                                                              Length 6904;
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Publication No. US20030003470A1
GENERAL INFORMATION:
APPLICANT: Salomen, Jukka T
TITLE OF INVENTION: Method for detecting a
                                                                                                                                                                                                                           SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 3
Query Match 81.6%;
Best Local Similarity 91.7%;
Matches 44; Conservative
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Best Local (
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                                                                                                                                                                                                                                                            FILE REFERENCE: 0933-0183P
CURRENT APPLICATION NUMBER: US/10/077,870
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: FI 20010323
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 10
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APPLICANT:
APPLICANT:
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APPLICANT: Valkonen, Vali-Pekka
APPLICANT: Valkonen, Vali-Pekka
TITLE OF INVENTION: A DNA molecule encoding a variant alpha-2B-adrenoceptor
TITLE OF INVENTION: protein, and uses thereof
FILE REFERENCE: Alpha-2B-AR variant
CURRENT APPLICATION NUMBER: US/09/825,923
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/422,985
PRIOR FILING DATE: 2000-05-25
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APPLICANT:
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                                                                                                                                                                                    LENGTH: 13
                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor
OTHER INFORMATION: protein
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                                                                                       PEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1350)
OTHER INFORMATION: Coding sequence for human alpha-2B-adrenoceptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                   ORGANISM: Homo sapiens
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Salonen, Jukka T
Salonen, Tomi-Pekka
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Salonen, Riitta
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91.7%;
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Score 41.6; DB 14;
Pred. No. 0.00075;
0; Mismatches 4;
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Pred. No. 0.00075;
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0; Mismatches
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                                 Length 1353;
   Indels
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Sequence 41, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1181
LENGTH: 2072
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                                                                                     US-10-225-567A-41
                                                                                                          RESULT 9
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                                                                                                                                                                                                                                                                                ; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g178197
US-10-305-720-1181
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US-10-305-720-1181
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APPLICANT: Brown, Joseph P.
             APPLICANT: LifeSpan Biosciences
                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                               Query Match
Best Local (
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Publication No. US20040010136A1

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression File Reference: pa.0002-1 CON

FILE REFERENCE: pa.0002-1 CON
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Best Local S
Matches 44
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CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/10001073
Publication No. US20030113725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Liggett, Stephen
APPLICANT: Small, Kirsten
TITLE OF INVENTION: Alpha-2-adrenergic receptor polymorphisms
FILE REFERENCE: 13073-PCT
                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                        4 GATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGTGTGAACCCCAG 51
                                                                                                                                                                                                                                44;
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                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                    81.6%; Score 41.6; DB 15;
91.7%; Pred. No. 0.00074;
ative 0; Mismatches 4;
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91.7%;
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Pred. No. 0.00075;
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APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
ITILE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-05
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR FILING DATE: 2001-08-05
RESULT 11
US-10-128-714-7204
; Sequence 7204, Application US/10128714
; Publication No. US20030119013A1
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Aspergillus fumigatus
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SOFTWARE: Patentin version 3.1
SEQ ID NO 6204
LENGTH: 2367
TYPE: DNA
                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
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Publication No. US20030119013A1
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LENGTH: 3274
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PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
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CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
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APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 81.6%; Local Similarity 91.7%;
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11 Similarity 88.6%;
39; Conservative
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Pred. No. 0.038;
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Pred. No. 0.00074;
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; ORGANISM: Aspergillus fumigatus US-10-128-714-204
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; TYPE: DNA
; ORGANISM: Aspergillus fumigatus
US-10-128-714-7204
                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR PPLICATION NUMBER: US 60/287,066
PRIOR PPLICATION NUMBER: US 60/287,066
PRIOR PILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR APPLICATION NUMBER: US 60/303,699
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
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CURRENT FILING DATE: 2002-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR FILING DATE: 2001-04-23
PRIOR PELLORION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: US 60/295,890
PRIOR APPLICATION NUMBER: US 60/303,899
PRIOR PILING DATE: 2001-07-09
PRIOR PILING DATE: 2001-07-09
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Best Local Similarity
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SEQ ID NO 7204
  Query Match
                                                                                                                                                         SEQ ID NO 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jiang, Bo
APPLICANT: Hu, Wengi
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Wethods of Use
FILE REFERENCE: 10182-018-999
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APPLICANT: Eroshkin, Alexey M
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/316,362 PRIOR FILING DATE: 2001-08-31
                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8603
                                                                                                                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/316,362
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                                                                                                         TYPE: DNA
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                                                                                                                                                                                    version
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                                                                                                                                                                                                                                     2001-08-31
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  70.6%; Score 36;
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Pred. No. 0.038;
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  BB
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Length 4238;
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APPLICANT: Leminut, Alexey M
APPLICANT: Lemieux, Sebastien M
ITITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
ITITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-999
[CURRENT APPLICATION NUMBER: US/10/128,714]
[CURRENT APPLICATION NUMBER: US 60/285,697]
[PRIOR APPLICATION NUMBER: US 60/285,697]
[PRIOR APPLICATION NUMBER: US 60/287,066]
[PRIOR APPLICATION NUMBER: US 60/287,066]
[PRIOR FILING DATE: 2001-04-23]
[PRIOR APPLICATION NUMBER: US 60/295,890]
[PRIOR APPLICATION NUMBER: US 60/295,890]
[PRIOR APPLICATION NUMBER: US 60/303,899]
[PRIOR APPLICATION NUMBER: US 60/30
                                                                                                                                                                                  APPLICANT: LA Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zoo Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other M
TITLE OF INVENTION: Plants and Uses Thereof for Plant Imp
FILE REPERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/89
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 139707
. ENDOTE: 1012
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; OTHER INFORMATION: Clone ID: US-10-424-599-139707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 8603
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                                                                                                TYPE: DNA
ORGANISM: Glycine max
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                                                                       FEATURE:
                                                                                                                                                                              LENGTH: 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3314 GAGGAGGAAGAAGAAGAGGAGGAGGAAGAGAGAGAGTTTGA 3357
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Tishkoff, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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88.6%;
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Pred. No. 0.03
0; Mismatches
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                                PAT_MRT3847_97163C.1
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US-10-424-599-94653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 16
US-09-864-408A-3111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: US/10/424,599
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 94653
LENGTH: 1554
TYPE: DNA
ORGANISM: Glycine max
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
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                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 9068
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 3111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Leach, Martin D.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, Richard A.
APPLICANT: Shimkets, US20040009474Alel Human Polynucleotides and Polypeptides Encounted Colorence Co
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 68.2%;
Similarity 84.8%;
       85
                                                                                                                                      1 Similarity
38; Conserv
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milarity 82.0%;
Conservative
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   ĠĀŖĠĀŢĠĀĠĠŖŖĠĀĀĠĀĠĠĀĠĠĀĠĠĀĠĠĀĠĠĀĀĠĀĀĠĀĠĀĀ 128
                                                         GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAAGAGTGTGA 44
                                                                                                                                         Conservative
                                                                                                                                                                                 67.5%;
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Pred. No. 0.051;
0; Mismatches 9;
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Pred. No. 0.0
                                                                                                                                                    Score 34.4; DB 11;
Pred. No. 0.12;
0; Mismatches 6;
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                                                                                                                                                                                                                                Length 392;
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RESULT 17

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US-10-191-803-61
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CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR FILING DATE: 2002-04-03
PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-05-06
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                                                                                                                                                                                                                                                                       APPLICANT: Match, Martin
APPLICANT: March, Martin
APPLICANT: Ren, Yongsheng
APPLICANT: Wu, Kuemei
APPLICANT: Wu, Kuemei
APPLICANT: Wu, Kuemei
APPLICANT: Wu, Kuemei
APPLICANTON: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
FILE REFERENCE: P01925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION UNMEER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION UNMEER: 60/106,020
PRIOR APPLICATION UNMEER: PCT/US99/25209
PRIOR FILING DATE: 1998-10-28
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 25
NUMBER OF SEQ ID NOS: 25
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US-09-844-864-12
; Sequence 12, Application US/09844864
; Patent No. US20020042926A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 1140
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 61
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APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, KOTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 44921-5090US
CURRENT APPLICATION NUMBER: US/10/191,803
CURRENT FILING DATE: 2002-07-10
                                                                                                                                                     US-09-844-864-12
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Best Local 9
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APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
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                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                            Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                          TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                   ENGTH: 182
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36 daadardacdaddaddaddaddaddaddaddaddaddaddardaa
                                1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGTGTGAA 45
                                                                                                   Similarity
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                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.5%;
                                                                                                       66.3%;
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                                                                                                       Score 33.8; DB 9;
Pred. No. 0.19;
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                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15;
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                                                                                                                                   Length 182;
                                                                                                   Indels
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US-10-424-599-108927
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                                                                                                     RESULT 21
US-10-369-493-27799
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; ORGANISM: Mus musculus
US-09-844-864-5
                                                                                                                                                                                                                                                                                                                                                   US-10-424-599-108927
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                                 Sequence 27799, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 108927
LENGTH: 2526
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                                                                                                                                                                                                                                                                 Best Local Similarity 84.4 Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 5
                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09844864 Patent No. US20020042926A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: La ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ren, Yongsheng
APPLICANT: WL, Xuemei
TITLE OF INVENTION: OVARY SPECIFIC GENES AND PROTEINS
FILE REFERENCE: PO1925US2 / 09807797 / OTA 99-48
CURRENT APPLICATION NUMBER: US/09/844,864
CURRENT FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR APPLICATION NUMBER: 60/106,020
PRIOR APPLICATION NUMBER: FCT/US99/25209
PRIOR APPLICATION NUMBER: PCT/US99/25209
PRIOR APPLICATION NUMBER: PCT/US99/25209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_69375C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
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les 38; Conserv
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Cao, Yong
Hinkle,
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Gregory J.
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                                                                                                                                                                                                                                                                                  Score 33.8; DB Pred. No. 0.18;
                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                            RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use of
FILE REFERENCE: WL-A-0.18201
CURRENT APPLICATION NUMBER: US/10/205,194
CURRENT FILING DATE: 5200-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 177
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SEQ ID NO 27799

LENGTH: 3401
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SEQ ID NO 145
                                                                                                                                           Patent No. US20020048763A1 GENERAL INFORMATION:
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Publication No.
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Best Local Similarity
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: "Hanzel, David K.
APPLICANT: Chen, Wensheng
TITHE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITHE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
PILE REFERENCE: Acomica-X-1
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APPLICANT: Lee, Kevin
APPLICANT: Dixon, Alistair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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o. US20030134301A1
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23

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PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PRILING DATE: 2000-09-27
PRIOR PRILING DATE: 2000-09-27
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR PELICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR PILING DATE: 2000-05-21 09/608,408
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-29
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
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OTHER INFORMATION: EXPRESSED IN FEITH LITTER, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN BLACENTA, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN ADULT LITER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BRAIN SIGNAL = 2.6
OTHER INFORMATION: SWISSPROT HIT: P51450, SYALUE 8.70e-02
OTHER INFORMATION: SWISSPROT HIT: P51450, SYALUE 8.70e-02
OTHER INFORMATION: SWISSPROT HIT: EXALUE 1.00e-36
OTHER INFORMATION: EST_HUMAN HIT: A1653251.1, EVALUE 2.00e-38
OTHER INFORMATION: EST_HUMAN HIT: A1653251.1, EVALUE 2.00e-38
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IOR APPLICATION NUMBER: GB 24263.6
RESULT 24
US-09-918-995-27029
US-09-918-995-27029, Application US/09918995
Sequence 27029, Application US20030073623A1
Publication No. US20030073623A1
GENERAL INFORMATION
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
TILING DATE: 2001-01-30
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92.1%;
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CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
LENGTH: 477
LENGTH: 477
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US-09-918-995-27029
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
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                                                    PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR PRIOR DATE: 2000-10-04
PRIOR PRIOR DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR PRILING DATE: 2001-01-30
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CURRENT FILING DATE: 2001-05-23
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PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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CATION NUMBER: US 09/608,408
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Pred. No. 0.
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.8
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                                                                                                                                             US-09-879-536-333
                                                                                                                                                                        RESULT 27
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; ORGANISM: Human
US-10-242-535A-43536
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TITLE OF INVENTION: Compositions and Methods Rel
FILE REFERENCE: 4211/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR PRILING DATE: 2001-07-13
PRIOR PRILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR PRILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-2
PRIOR FILING DATE: 2001-03-2
PRIOR FILING DATE: 2001-03-2
PRIOR FILING DATE: 2001-03-2
PRIOR PRILING DATE: 2001-03-2
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Best Local S
Matches 35
Sequence 333, Application US/09879536
PATENT NO. US20020144298A1
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.2
SEQ ID NO 43536
LENGTH: 390
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Best Local Similarity
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 6378
                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 AGGAGGAAGAGGAGGAGGAGGAGGAGGAAGAG 404
                                                                                                                                                                                                                                                                                                                                               39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGATGAAGCTGAAGAGGAGGAGGAGGAGGAAGAG 39
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                   64.7%;
79.6%;
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Pred. No. 0.32;
0; Mismatches
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Pred. No. 0.28;
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                                                                                                                                                                                                                                                                                                                                                                                         DB 15;
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APPLICANT: Lewis, Marcia E.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS

FILE REFERENCE: CCD-257 (US)

CURRENT APPLICATION NUMBER: US/09/879,536

CURRENT PILING DATE: 2001-09-21

PRIOR APPLICATION NUMBER: US 60/088,801

PRIOR FILING DATE: 1998-06-10

NUMBER OF SEQ ID NOS: 850

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 333

LENGTH: 650

Type: Number 650
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US-09-879-536-333
RESULT 29
                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT3847_25349C. US-10-424-599-60174
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                                                                                                                                                                                                                                                                                                       SEQ ID NO 60174
                                                                                                                          Best 'Local
Matches
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53223)B
FILE REFERENCE: 38-21 (53223)B
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Best Local Similarity
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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APPLICANT:
APPLICANT:
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NAME/KEY: misc_feature
LOCATION: (1)...(650)
                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                      LENGTH: 1634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCC
                                                                          1 GAGGATGAAGCTGAAGAGGAGGAGGAGGAGGAGGAGGAGTGTGAACCCCC
                                                                                                                          39;
                                                                                                                                           Similarity
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Ford, Donna M.
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Bushnell, Steven E.
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                                                                                                                          Conservative
                                                                                                                                         64.7%;
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                                                                                                                        Score 33; DB 12; Length 1634; Pred. No. 0.32; O; Mismatches 10; Indels
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US-10-029-386-18468; Sequence 18468, Application US/10029386; Publication No. US20030194704A1